Prevalence of *BRCA1* and *BRCA2* pathogenic variants in a large, unselected breast cancer cohort

Original research

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RUNNING TITLE

BRCA testing for all newly-diagnosed breast cancer patients?

DISCLOSURE OF POTENTIAL CONFLICT OF INTEREST

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ABSTRACT

Breast cancer patients with *BRCA1/2*-driven tumors may benefit from targeted therapy. It is not clear whether current *BRCA* screening guidelines are effective at identifying these patients. The purpose of this study was to evaluate the prevalence of inherited *BRCA1/2* pathogenic variants in a large, clinically representative breast cancer cohort and to estimate the proportion of *BRCA1/2* carriers not detected by selectively screening individuals with the highest probability of being carriers according to current clinical guidelines. The study included 5,122 unselected Swedish breast cancer patients diagnosed from 2001 to 2008. Target sequence enrichment (48.48 Fluidigm Access Arrays) and sequencing were performed (Illumina Hi-Seq 2500 instrument, v4 chemistry). Differences in patient and tumor characteristics of *BRCA1/2* carriers who were already identified as part of clinical *BRCA1/2* testing routines and additional *BRCA1/2* carriers found by sequencing the entire study population were compared using logistic regression models. Ninety-two of 5,099 patients with valid variant calls were identified as *BRCA1/2* carriers by screening all study participants (1.8%). Only 416 study participants (8.2%) were screened as part of clinical practice, but this identified 35 out of 92 carriers (38.0%). Clinically-identified carriers were younger, less likely postmenopausal and more likely to be associated with familiar ovarian cancer compared to the additional carriers identified by screening all patients. More *BRCA2* (34/42, 81.0%) than *BRCA1* carriers (23/50, 46%) were missed by clinical screening. In conclusion, *BRCA1/2* mutation prevalence in unselected breast cancer patients was 1.8%. Six in ten *BRCA* carriers were not detected by selective clinical screening of individuals.

NOVELTY AND IMPACT

This is one of the largest studies on *BRCA1/2* prevalence in an unselected breast cancer population.

INTRODUCTION

Estimates of the prevalence of *BRCA1* or *BRCA2* germline pathogenic variants vary considerably depending on the technology used for mutation screening, population size, and to what extent the genes are tested [1]. Although *BRCA1/2* pathogenic variants are major determinants of hereditary breast cancers, women diagnosed with *BRCA1/2*-associated breast cancer do not necessarily exhibit worse survival patterns than breast cancer patients without such pathogenic variants [2]. On the contrary, patients diagnosed with *BRCA1/2*-associated breast cancers have advantages in terms of treatment options when compared to patients with *BRCA1/2* wild-type breast cancer (reviewed in [3]). Evidence from clinical trials showed significantly greater sensitivity and higher response rate of *BRCA1/2*-associated cancers to neoadjuvant and standard adjuvant chemotherapy than their wild-type *BRCA1/2* counterparts [3]. Treatment options for *BRCA1/2* breast cancers are also broadened with the introduction of new therapeutic agents, such as poly (ADP-ribose) polymerase (*PARP*) inhibitors, which selectively target *BRCA1/2*-deficient cancer cells [4-7].

Recommendation for counselling and genetic screening for *BRCA1/2* pathogenic variants is mainly based on personal and family history of breast and/or ovarian cancer, young age at disease onset, male breast cancer and multiple tumors (bilateral breast cancer or breast and ovarian cancer in the same patient) [8]. However, *BRCA* testing guidelines vary by region and country [9, 10]. In Sweden, the Swedish Breast Cancer Group *BRCA1* and *BRCA2* screening criteria are used [8]. A report by Nilsson *et al*. estimated that the Swedish *BRCA* testing criteria has an effectiveness of only 18% and concluded that clinical genetic testing criteria for *BRCA1* and *BRCA2* should be critically revised [8]. As the effective identification of *BRCA1*/*2* germline pathogenic variants has potential to influence treatment decision and has implications for the family of the patients [3-6, 11, 12], the pros and cons of testing all women diagnosed with breast cancer for such pathogenic variants need to be examined. In a large, clinically representative breast cancer cohort, we examined the prevalence and characteristics of *BRCA1/2* germline mutation carriers and compared our results with *BRCA* mutation carriers already identified through a national clinical *BRCA* screening program.

METHODS

Study participants

All women under the age of 80 and diagnosed with breast cancer from 2001 to 2008 in Stockholm, Sweden were identified through the Stockholm-Gotland Regional Breast Cancer quality register [13, 14]. Women were invited to participate in the LIBRO1 study in 2009. In all, 5,715 women of the LIBRO1 study gave informed consent to the retrieval of data from medical records and national registers, answered a detailed questionnaire on background and lifestyle risk factors, and provided a blood specimen for genetic analysis [13, 14]. Of these women, 5,125 were successfully genotyped in a large-scale genotyping study on breast cancer risk (see **eTable 1** in **Data Supplement 1** for exclusion criteria, online only) [15]. Of these women, 5,122 had enough DNA remaining for targeted sequencing. The final analytical dataset comprised 5,099 samples which passed quality control. This study was approved by the Regional Ethical Review Board in Stockholm, Sweden (Karolinska Institutet, DNR2009/254-31/4).

Patient characteristics

Self-reported information on education level, age at menarche, body mass index (BMI), number of children, oral contraceptive use, hormone replacement therapy, and details of family history of breast and ovarian cancer were obtained from the questionnaire. Patients were asked if their biological mothers and sisters have been diagnosed with breast or ovarian cancer, and if so, at what age. Mammograms were retrieved from radiology departments. Percent mammographic density was measured using an automated method described in [16]. Information on whether the patients have an ovarian cancer or any non-breast malignancy was retrieved via linkage to the Swedish Cancer Register using unique personal identity numbers of study participants (*personnummer*, ten or twelve digit number used in Sweden to identify individuals) [17].

Tumor characteristics

Tumor characteristics were retrieved from the Stockholm-Gotland Regional Breast Cancer Quality Register [18, 19] using unique personal identity numbers [17]. Tumor size was measured in millimetres. Lymph node involvement was dichotomized into positive or negative. Estrogen receptor (ER) status was recorded as negative or positive in the registers, determined by radioimmunoassay or

immunohistochemistry with cutoff values of more than 10% positive cells for IHC and more than 0 fmol/µg DNA for radioimmunoassay assays. The completeness of the registry data was 98% for tumor size and lymph node status and 80% for ER status. Information on grade (Nottingham histologic grade for invasive cancer and nuclear grade for cancer *in situ*) was available from 2004, with 93% completeness [19].

Data on molecular markers were retrieved in 2015–2016 from medical and pathology records at treating hospitals (previously described in [20]). HER2 status was dichotomized (positive/negative) in accordance with the Swedish Society of Pathology's guidelines: negative if protein expression showed 0 or 1+, or was higher with no confirmed gene amplification by FISH, and positive if FISH showed gene amplification.[20] Proliferation marker Ki67 was measured according to contemporary guidelines and reported as percent staining (low if <20% and high otherwise).[20] HER2 and Ki67 markers were not assessed, and thus not available in medical records, prior to 2005. Breast cancer subtype was assigned using a random forest algorithm (caret R package, v. 6.0.58) described in [20]. The algorithm was trained to predict subtype based on a subset of individuals with PAM50 subtype derived from gene expression data (*n*=237). Breast cancer subtype was then assigned to the remaining cases based on age at diagnosis, ER, PR, HER2, and Ki67 status.

Targeted sequencing and data processing

Target-enriched sequencing libraries of germline DNA from 5,122 breast cancer patients were prepared at the Centre for Cancer Genetic Epidemiology (University of Cambridge), as part of a larger effort that included samples from other cohorts. Briefly, target sequence enrichment was performed using 48.48 Fluidigm Access Arrays according to the manufacturer's protocol (Fluidigm, South San Francisco, California, USA). Fluidigm D3 assay design software was used to select primer pairs, which were multiplexed into pools selected for GC content and avoidance of off-target primer-primer and primer-product complementarity (**eTable 2** in **Data Supplement 2**). Target sequences were amplified with Illumina sequencing adaptors and one of 1,536 unique sample barcodes (supplied by Fluidigm, South San Francisco, California, USA). Robotic liquid handling and barcode plate identification were used in all steps of the library preparation process. The amplicon library was quantified with the KAPA Library Quantification Kit (KapaBiosystems, Boston, Massachusetts, USA) and then sequenced on the Illumina Hi-Seq 2500 instrument using v4 chemistry, according to the

manufacturer's protocol (Illumina, San Diego, California, USA). Each library was sequenced 2-3 times to provide sufficient coverage. Details on sequence data processing and quality control are shown in **eMethods** in **Data Supplement 1**. A total of 5,099 samples had valid variant calls. The mean read depth across the coding sequences of *BRCA1* and *BRCA2* was 792.2 (standard deviation: 587.4) and 631 (standard deviation: 516), respectively. More than 90% of targeted bases had more than 15x coverage (94.8 [15.9] and 92.5 [20.4] for *BRCA1* and *BRCA2*, respectively).

Definition of pathogenic variants

As described previously in Borg *et al*. [21], sequence variants were categorized based on their predicted effect on the mRNA and amino acid level and defined as pathogenic if they were (1) frameshift and nonsense variants with the exception of the *BRCA2* c.9976A>T (BIC: K3326X) and other variants located 3' thereof (*n*=105), and (2) all consensus splice acceptor or donor sequence sites, except those predicted to lead to naturally occurring in-frame RNA isoforms that may rescue gene function [22]. Public data on pathogenic *BRCA* variants (includes frameshift insertion/deletions, nonsense, splice sites and missense variants conclusively demonstrated to be pathogenic) that have been curated and classified by an international expert panel, the ENIGMA consortium, were also downloaded from http://brcaexchange.org/ (access date: Feb 22, 2017) for the annotation of the sequence data.

Identification of women who have undergone *BRCA* testing in Sweden

Mutation screening for all oncogenetic clinics in Sweden (Lund, Stockholm, Uppsala, Göteborg, Linköping and Umeå) were conducted at the Department of Oncology, Lund University as part of a national *BRCA* testing program (**eMethods** in **Data Supplement 1**). We cross-referenced the personal identity numbers of all study participants in LIBRO1 with the *BRCA* testing unit at Lund University to identify women who have been tested for *BRCA1/2* pathogenic variants previously. The SweBRCA criteria are the only *BRCA1/2* testing criteria used in Sweden (**eTable 3** in **Data Supplement 1**) [8]. Clinicians do not have any obligation to comply with the guidelines [8].

Statistical analysis

Predictor variables which include patient and tumor characteristics were described by the counts of each category and corresponding proportions. Binary logistic regression models were fitted

for the dichotomous outcome (*BRCA1* [reference] and *BRCA2*), and multinomial logistic regression models were fitted for the three-category outcome (*BRCA1*, *BRCA2* and non-*BRCA* [reference category]), adjusting for age and year of diagnosis. Logistic regression models were also used to compare estimates (odds ratios [OR] and corresponding 95% confidence intervals [CI]) of patient and tumor characteristics between *BRCA1/2* carriers already identified among a subset of 416 patients screened as part of clinical *BRCA* testing routines and additional *BRCA1/2* carriers found by sequencing the entire study population (i.e. those not tested by the Swedish *BRCA* testing program).

RESULTS

The median time from date of diagnosis to study entry is 4.8 years (range: 1.3 to 9.2). The median age of breast cancer diagnosis of the study cohort was 59.6 years (range: 25.1 to 79.9). Nine of ten breast cancers were invasive (89.4%).

Spectrum of *BRCA1* and *BRCA2* pathogenic variants

Of the 5,099 breast cancer patients, 92 (1.8%) were identified as *BRCA1/2* carriers (50 *BRCA1* carriers and 42 *BRCA2* carriers) and 5,007 were non-*BRCA*.

Among the 50 *BRCA1* carriers, there were 28 unique germline *BRCA1* pathogenic variants (11 frameshift deletions, 2 frameshift insertions, 8 truncating, 4 splice sites, and 3 missense) (**Figure 1** and **eTable 4** in **Data Supplement 1**). Frameshift insertions and deletions made up 26/50 (52%) of the *BRCA1* pathogenic variants. Exon 11 harbored 33/50 (66%) of the *BRCA1* pathogenic variants. The most common pathogenic variant was c.3048_3052dupTGAGA (*n*=8), which is a founder mutation originating from the West coast of Sweden [23]. Three other Swedish founder pathogenic variants were also identified (c.1082_1092del [*n*=5], c.2475delC [*n*=2]) and c.3626delT [*n*=3]) [23-26].

Among the 42 *BRCA2* carriers, there were 33 unique *BRCA2* pathogenic variants (18 frameshift deletions, 3 frameshift insertions, 9 truncating, and 3 splice sites) (**Figure 2** and **eTable 5** in **Data Supplement 1,** only online). Over half of all *BRCA2* carriers (24/42, 57.1%) had a pathogenic variant on exon 11.

Patient characteristics of *non-BRCA*, *BRCA1* and *BRCA2* carriers

Half of the non-*BRCA* women were at least 60 years old, compared to 26.0% and 33.3% for women with *BRCA1* and *BRCA2* pathogenic variants, respectively (**eTable 6** in **Data Supplement 1**).

In the crude analyses controlling for age and year of diagnosis, *BRCA1* and *BRCA2* carriers were more likely than non-*BRCA* women to report family history of both breast ($OR_{BRCA1 \text{ vs non-}BRCA}$: 4.00 [2.27 to 7.05] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 2.23 [1.17 to 4.26]) and family history of ovarian cancer ($OR_{BRCA1 \text{ vs non-}BRCA}$: 7.53 [3.82 to 14.82] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 3.62 [1.50 to 8.71]) (**eTable 6** in **Data Supplement 1**). *BRCA1* carriers, in particular, were also more likely to be also diagnosed with an ovarian cancer themselves ($OR_{BRCA1 \text{ vs non-}BRCA}$: 28.02 [10.72 to 73.29] and $OR_{BRCA2 \text{ vs non-}BRCA}$: 8.11 [1.87 to 35.24]) than non-*BRCA* patients (**eTable 6** in **Data Supplement 1**). *BRCA1* carriers were more likely to have a personal history of another malignant cancer in addition to their breast cancer than patients with non-*BRCA* patients ($OR_{BRCA1 \text{ vs non-}BRCA}$: 2.93 [1.37 to 6.27]). This association was driven by ovarian cancers ($OR_{BRCA1 \text{ vs non-}BRCA}$ for all non-breast and non-ovarian malignancies: 0.83 [0.25 to 2.73]). *BRCA2* carriers were significantly less likely to be ever users of hormone replacement therapy (HRT) than non-*BRCA* breast cancer patients (26.2% vs 53.8%) (**eTable 6** in **Data Supplement 1**). In multivariable models shown in **Table 1**, all variables remained significantly associated, with the exception of personal history of any non-breast malignancy.

Tumor characteristics of *non-BRCA*, *BRCA1* and *BRCA2* carriers

In the crude analyses controlling for age and year of diagnosis, *BRCA2* carriers were in general not significantly different from non-*BRCA* women in terms of tumor characteristics, with the exception of nodal involvement ($OR_{BRCA2 \text{ vs non-}BRCA}$: 2.71 [1.31 to 5.62], **eTable 7** in **Data Supplement 1**). On the contrary, tumors of *BRCA1* carriers were more aggressive than those of non-*BRCA* breast cancer patients for all tumor characteristics examined (ER and PR status, grade, tumor size, nodal involvement, and breast cancer subtype) except for the proportion of invasive tumors (**eTable 7** in **Data Supplement 1**).

In multivariable multinomial models including all tumor characteristics that were significantly different between non-*BRCA* and *BRCA1*-positive breast cancer patients, only ER-negativity remained significant ($OR_{BRCA1 \text{ vs non-}BRCA}$: 5.19 [2.68 to 10.06]) (**Table 1**). ER status was also the only independent tumor characteristic that distinguished between *BRCA1* and *BRCA2* carriers ($OR_{BRCA2 \text{ vs } BRCA1}$: 0.22 [0.07 to 0.77]). This observation was mirrored in a separate multinomial model considering breast cancer subtypes, where *BRCA1* tumors were found to be 40 times more likely to be of the basal-like subtype ($OR_{BRCA1 \text{ vs non-}BRCA}$: 40.07 [14.26 to 112.59]). Only nodal involvement remained

significant in the comparison between *BRCA2* and non-*BRCA* breast cancer cases in the multivariable model ($OR_{BRCA2 \text{ vs non-}BRCA}$: 2.54 [1.20 to 5.37) (**Table 1**).

Comparison of *BRCA1/2* carriers identified versus not identified through clinical screening

Linkage with the Swedish *BRCA* register found 416 patients (8.2%) that were screened for pathogenic variants as part of routine clinical practice. Among these 416 women, clinical screening identified 39 carriers in the study cohort, of which our study confirmed 35 (**Figure 3**). Four pathogenic variants were missed (*BRCA1*: c.4186-1785_4358-1667dup and c.4358-1729_4986+736dup; *BRCA2*: c.7805+1538_8331+560del and c.9097_9098insT) (**Figure 3**). Three of these were large exonic deletions or duplications that the Fluidigm Access Array system is not suitable for detecting. This gives the Fluidigm Access Array method an estimated sensitivity of about 90%, or 97% when excluding large exonic variants.

Overall, 57/92 carriers (62.0%) were not already clinically identified: Two additional carriers were detected by the Fluidigm Access Array method among clinically screened patients (*BRCA2*: c.2578delA [confirmed by Sanger sequencing to be a false positive] and c.7443delT [missed carrier, screened with DHPLC and MLPA in 2008]); the remaining 55 out of 92 carriers (59.8%) identified by the Fluidigm Access Array method in the complete study cohort were never screened as part of clinical routine (**Figure 3**).

More *BRCA2* (34/42, 80%) than *BRCA1* pathogenic variants (23/50, 46%) were missed by selectively testing only high-risk individuals who were recommended for genetic testing and counselling (**Table 2**). Controlling for only year of diagnosis, *BRCA* carriers identified by clinical routine screening were younger (37.2% aged 50 years and above, compared to 73.7%), less likely to have experienced menopause ($OR_{\text{identified versus not identified}}$: 0.17 [0.07 to 0.44]) and more likely to be associated with a family history of ovarian cancer ($OR_{\text{identified versus not identified}}$: 3.11 [1.06 to 9.09]) (**Table 2**). Further adjustment for gene revealed a significant association with age at menarche ($OR_{\text{identified versus not identified}}$: 2.99 [1.00 to 8.94]). There was also a trend between the likelihood of being identified as a carrier by selective testing and more children (**Table 2**). Tumors of *BRCA1/2* carriers identified by selective testing were more often detected clinically ($OR_{\text{identified versus not identified}}$: 5.52 [1.38 to 22.18]), higher grade ($OR_{\text{identified versus not identified}}$: 0.28 [0.08 to 0.92]), larger size ($OR_{\text{identified versus not identified}}$: 2.48 [1.00 to 6.16]) and of a basal subtype ($OR_{\text{identified versus not identified}}$: 6.07 [1.49 to 24.76]) (**eTable 8** in **Data**

Supplement 1). The differences observed for all tumor characteristics and selective testing detection did not remain significant after adjusting for gene.

DISCUSSION

BRCA1/2 pathogenic variants were found in 1.8% of unselected breast cancer patients. In contrast to studies reporting *BRCA1/2* prevalence for a subset of high risk women [27, 28], the present sample reflects the general breast cancer population. None of the breast cancer risk factors examined differed between *BRCA1* and *BRCA2* carriers. However, *BRCA1* and *BRCA2* breast cancers differed in the proportions of patients with ER-negative disease and basal-like subtype. Six out of ten *BRCA1/2* carriers were not identified through genetic testing in the clinic.

BRCA1 and *BRCA2* mutation frequencies in breast and ovarian cancer patients unselected for family history or age at onset are generally low (<1–7% for *BRCA1* and 1–3% for *BRCA2*) [29]. The combined *BRCA1/2* mutation frequency in a Swedish population of unselected breast cancer cases recruited from 1998 through 2000 in Stockholm has been previously estimated to be not more than 1% in the work by Margolin *et al*. [1]. In that study, screening for *BRCA1* pathogenic variants was limited to exon 11, which covers over half the coding region of *BRCA1* [30]. More than 70% of diagnosed pathogenic variants including four founder pathogenic variants in the Swedish population are known to be located on this exon [31-33]. Prevalence of *BRCA2* pathogenic variants in the Swedish population was deemed by Margolin *et al*. to be negligible among unselected breast cancer patients due to the low frequency of such pathogenic variants even in high-risk groups in the region [1]. On the contrary, only 33 of 50 *BRCA1* pathogenic variants were identified on exon 11 in this study, thus suggesting that 34% of *BRCA1* carriers would have been missed if exon 11 alone were screened. Through testing the entire sequences of *BRCA1/2* genes with improved methodology and techniques, we estimate the combined prevalence of *BRCA1/2* pathogenic variants among unselected breast cancer patients in Sweden to be closer to 2%.

There are close to 2,000 known *BRCA1* germline pathogenic variants, many of which are loss-of-function frameshift pathogenic variants [34]. Nine of 28 (32%) unique *BRCA1* and 6 of 33 (18%) unique *BRCA2* pathogenic variants were found to be recurrent in Swedish breast cancer patients (i.e. pathogenic variants that were found to occur in at least two unrelated individuals). The relatively low recurrent mutation frequency, including that of Swedish founder pathogenic variants, would mean that

screening of selected pathogenic variants alone may not be a sensitive approach in this population as majority of *BRCA1* and *BRCA2* carriers will have been missed. While *BRCA1* pathogenic variants confer a more aggressive tumor phenotype, *BRCA2* pathogenic variants typically resemble sporadic breast cancer [35]. There is good agreement between our observed results regarding the tumor characteristic differences between *BRCA1/2* and non-*BRCA* breast cancer cases and what has been previously reported in literature. It has been observed by others that tumors in *BRCA1* carriers more frequently exhibited high mitotic count, high grade, ER and PR negativity [36-38]. A large proportion of *BRCA1* mutation cases (~80%) have also been documented to be triple negative and basal-like breast cancers [36-38]. In a Swedish study where 54 female breast cancer patients from 22 families with *BRCA2* germ line pathogenic variants from Sweden and Denmark were compared with 214 age- and date of diagnosis-matched controls identified among breast cancer patients from South Sweden, *BRCA2*-associated cases were more often node-positive than non-*BRCA* cases [39]. Other than nodal involvement, *BRCA2*-associated breast carcinomas were generally associated with less aggressive tumor characteristics than *BRCA1* cancers, and were more likely to be hormone-related [37, 38].

Thirty-eight percent of *BRCA1/2* carriers were identified through selective clinical testing of 8.2% of breast cancer patients. Grindedal *et al.* evaluated the results of *BRCA1/2* testing in South-Eastern Norway and found that 65% of the *BRCA1/2* carriers would have been missed if using age of onset below 40 or triple negative breast cancer as criteria for testing [40]. It is also conceivable that, due to an emphasis on disease family history in current guidelines, a smaller family size may compromise the identification of high risk individuals who would otherwise benefit from genetic testing [41]. In a Swedish retrospective study by Nilsson *et al*. where all breast cancer patients were tested, it was found that while 65% of the *BRCA1/2* carriers fulfilled Swedish criteria for testing, only 18% had been identified in regular clinical routine [8]. Other factors such as varying compliance with guidelines for the recommendation of *BRCA* testing by clinicians will lead to even more *BRCA1/2* carriers being missed. It may thus be of benefit to test all newly diagnosed breast cancers in light of available targeted therapy options.

To our knowledge, this is the largest population-based breast cancer testing study for *BRCA1/2* published outside of founder populations. Despite the richness of the data which encompasses patient and tumor, some risk groups were too small to be examined with adequate statistical power (e.g. benign breast disease). The Swedish health care system is mainly government-

funded and decentralized, making it possible to identify all women who went for clinical *BRCA* testing. Nonetheless, private health care also exists, and some *BRCA1/2* carriers may have been identified by commercial testing outside the public sector. However, the number of patients tested outside of the national *BRCA* testing program is likely negligible during the period 2001-2008 [8]. It should be also noted that the Fluidigm Access Array method used cannot detect large rearrangements and has a sensitivity of ~90%, hence further analytical validity studies are needed. More sensitive methods and the universal *BRCA* testing of newly breast cancer patients will help to increase the number of women getting the best treatment for their disease.

In summary, *BRCA1/2* pathogenic variants were found in 1.8% of an unselected Swedish breast cancer cohort. Six out of ten *BRCA* carriers were not identified through selective clinical testing routines. Our results give fruitful information for further decisions of *BRCA* testing for all breast cancer patients at time of diagnosis. The presented data can be a starting point for further studies dealing with issues such as cost effectiveness of screening patients with different tumor characteristics and patient health attitudes.

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FIGURE LEGENDS

Figure 1. Mutation plots of *BRCA1*. Four and three splice variants for *BRCA1* (NM_007294.3) are not shown.

Figure 2. Mutation plots of *BRCA2*. Three splice variants for *BRCA2* (NM_000059.3) are not shown.

Figure 3. Overlap between women attending *BRCA* screening (clinically tested), *BRCA* carriers identified through selective clinical testing routine (clinically-detected carriers), and *BRCA* carriers identified through screening all unselected LIBRO1 breast cancer patients (unselected-detected). Of the 416 women who were clinically tested, 39 were found to be *BRCA1/2* carriers (39/416, 9.3%). Our study confirmed 35 of these pathogenic variants. Four pathogenic variants were missed (*BRCA1*: c.4186-1785_4358-1667dup and c.4358-1729_4986+736dup; *BRCA2*: c.7805+1538_8331+560del and c.9097_9098insT). By sequencing the entire Swedish study, we found 55 more carriers who were not screened as part of clinical routine.

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Table 1. Odds ratio (OR) and corresponding 95% confidence intervals (CI) of predictors according to *BRCA* status.

	BRCA1 vs non-BRCA **OR (95% CI)**	***BRCA2 vs non-BRCA*** **OR (95% CI)**	***BRCA2 vs BRCA1*** **OR (95% CI)**
Model 1: Patient characteristics			
Age at diagnosis: 50-59	**0.21 (0.10 to 0.45)**	0.78 (0.36 to 1.69)	**3.55 (1.05 to 11.97)**
Age at diagnosis: ≥60	**0.14 (0.06 to 0.31)**	0.55 (0.24 to 1.23)	**3.91 (1.11 to 13.84)**
Year of diagnosis: 2005-2008	1.68 (0.91 to 3.08)	1.03 (0.55 to 1.92)	0.90 (0.33 to 2.48)
HRT ever: Yes	1.08 (0.56 to 2.10	**0.36 (0.17 to 0.76)**	**0.31 (0.10 to 0.93)**
Familiy history of breast cancer: Yes	**3.57 (1.99 to 6.41)**	**2.08 (1.08 to 3.99)**	0.60 (0.24 to 1.55)
Familiy history of ovarian cancer: Yes	**6.99 (3.43 to 14.24)**	**3.57 (1.47 to 8.68)**	0.38 (0.11 to 1.35)
Personal history of ovarian cancer: Yes	**19.21 (5.89 to 62.72)**	**8.01 (1.61 to 39.94)**	0.49 (0.04 to 6.74)
Personal history of any malignant cancer (not breast): Yes	1.35 (0.52 to 3.54)	0.81 (0.26 to 2.56)	0.49 (0.07 to 3.59)
Model 2: Tumor characteristics, adjusted for age and year of diagnosis			
Detection mode: Interval	1.34 (0.38 to 4.79)	1.16 (0.45 to 3.03)	0.44 (0.05 to 3.50)
Detection mode: Clinical cancer in women without previous mammograms	2.61 (0.81 to 8.37)	0.66 (0.20 to 2.12)	0.35 (0.05 to 2.38)
Detection mode: Clinical cancer in women who had previous mammograms (i.e. interval >24 months)	**3.54 (1.15 to 10.89)**	1.57 (0.63 to 3.94)	0.34 (0.06 to 2.02)
ER status: Negative	**5.19 (2.68 to 10.06)**	1.17 (0.48 to 2.87)	**0.22 (0.07 to 0.77)**
Grade: Intermediate-differentiated	1.97 (0.24 to 16.23)	1.82 (0.52 to 6.34)	1.32 (0.10 to 18.26)
Grade: Poorly-differentiated	7.11 (0.91 to 55.30)	1.55 (0.39 to 6.22)	0.36 (0.03 to 4.92)
Tumor size: ≥20	0.87 (0.48 to 1.59)	1.26 (0.67 to 2.39)	1.17 (0.37 to 3.76)
Nodal involvement: Yes	1.60 (0.79 to 3.27)	**2.54 (1.20 to 5.37)**	1.67 (0.43 to 6.51)
Model 3: Breast cancer subtype, adjusted for age and year of diagnosis			
Subtype: Luminal B	2.83 (0.54 to 14.77)	0.49 (0.06 to 3.73)	0.19 (0.01 to 2.60)
Subtype: HER2-enriched	0.93 (0.11 to 8.07)	0.33 (0.04 to 2.52)	0.38 (0.02 to 8.07)
Subtype: Basal-like	**40.07 (14.26 to 112.59)**	0.84 (0.11 to 6.43)	**0.02 (0.00 to 0.17)**

Table 2. Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of patient characteristics among *BRCA* carriers identified versus not identified through selective clinical screening.
* Adjusted for year of diagnosis (2001-2004, 2005-2008). † Adjusted for year of diagnosis and gene (*BRCA1*, *BRCA2*). ‡ Adjust for year of diagnosis, gene and age at diagnosis (<50, 50-59, ≥60).

Patient characteristic	Not identified by selective testing (*n*=57) *n* (%)	Identified by selective testing (*n*=35) *n* (%)	OR (95% CI)*	OR (95% CI)†	OR (95% CI)‡
Gene, *unadjusted					
BRCA1	23 (40.4)	27 (77.1)	1.00 (Reference)		
BRCA2	34 (59.6)	8 (22.9)	**0.20 (0.08 to 0.52)**		
Age at diagnosis, *unadjusted					
<50	15 (26.3)	22 (62.9)	1.00 (Reference)		
50-59	20 (35.1)	8 (22.9)	**0.27 (0.10 to 0.78)**		
≥60	22 (38.6)	5 (14.3)	**0.15 (0.05 to 0.50)**		
Year of diagnosis, *unadjusted					
2001-2004	26 (45.6)	12 (34.3)	1.00 (Reference)		
2005-2008	31 (54.4)	23 (65.7)	1.61 (0.67 to 3.84)		
Education					
University	29 (50.9)	21 (60.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Intermediate	12 (21.1)	9 (25.7)	1.06 (0.37 to 2.98)	1.40 (0.45 to 4.39)	2.08 (0.59 to 7.40)
Elementary	7 (12.3)	0 (0.0)	-	-	-
Other	9 (15.8)	5 (14.3)	0.78 (0.23 to 2.68)	0.65 (0.17 to 2.46)	1.63 (0.35 to 7.66)
Age at menarche in years					
<13	21 (36.8)	7 (20.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥13	36 (63.2)	28 (80.0)	2.17 (0.79 to 5.94)	**2.99 (1.00 to 8.94)**	**4.12 (1.19 to 14.26)**
Menopause status before breast cancer diagnosis					
Premenopause	14 (24.6)	23 (65.7)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Postmenopause	43 (75.4)	12 (34.3)	**0.17 (0.07 to 0.44)**	**0.17 (0.06 to 0.45)**	0.18 (0.03 to 1.25)
BMI in kg/m^2					
<25	29 (50.9)	24 (68.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥25	27 (47.4)	11 (31.4)	0.52 (0.21 to 1.27)	0.42 (0.16 to 1.12)	**0.32 (0.11 to 0.94)**
Missing	1 (1.8)	0 (0.0)			
Percentage mammographic density					
<25	22 (38.6)	10 (28.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥25	16 (28.1)	14 (40.0)	1.97 (0.69 to 5.62)	1.54 (0.51 to 4.69)	0.93 (0.27 to 3.21)
Missing	19 (33.3)	11 (31.4)			
Number of children					
0	12 (21.1)	3 (8.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
1	13 (22.8)	7 (20.0)	2.39 (0.49 to 11.65)	2.64 (0.50 to 13.83)	5.34 (0.84 to 33.79)
2	22 (38.6)	14 (40.0)	2.91 (0.68 to 12.53)	3.12 (0.68 to 14.24)	4.76 (0.89 to 25.43)
≥3	10 (17.5)	11 (31.4)	4.64 (1.00 to 21.66)	4.69 (0.93 to 23.60)	**10.55 (1.62 to 68.68)**
HRT ever					
No	34 (59.6)	25 (71.4)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	21 (36.8)	10 (28.6)	0.61 (0.24 to 1.54)	0.45 (0.16 to 1.24)	0.84 (0.26 to 2.70)
Missing	2 (3.5)	0 (0.0)			
Oral contraceptives ever					
No	19 (33.3)	5 (14.3)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	37 (64.9)	30 (85.7)	3.04 (1.01 to 9.15)	2.90 (0.91 to 9.24)	2.36 (0.71 to 7.85)
Missing	1 (1.8)	0 (0.0)			
Family history of breast cancer					
No	37 (64.9)	18 (51.4)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	20 (35.1)	17 (48.6)	1.84 (0.77 to 4.39)	1.58 (0.63 to 3.99)	1.46 (0.54 to 3.90)

Family history of ovarian cancer					
No	50 (87.7)	24 (68.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	7 (12.3)	11 (31.4)	**3.11 (1.06 to 9.09)**	2.87 (0.91 to 9.11)	3.41 (0.99 to 11.73)
Ovarian cancer					
No	51 (89.5)	33 (94.3)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	6 (10.5)	2 (5.7)	0.60 (0.11 to 3.26)	0.37 (0.06 to 2.17)	0.46 (0.07 to 3.01)
Other malignant cancer					
No	48 (84.2)	31 (88.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	9 (15.8)	4 (11.4)	0.76 (0.21 to 2.75)	0.54 (0.14 to 2.12)	0.66 (0.15 to 2.96)

Prevalence of *BRCA1* and *BRCA2* pathogenic variants in a large, unselected breast cancer cohort

DATA SUPPLEMENT 1

eTable 1. Exclusion criteria for genotyping experiment (Michailidou *et al.* [1]). Of the 5,715 women who consented to genetic analyses of their blood samples, genotyping was successfully performed for 5,125 women. Of these, 5,122 had enough DNA remaining for targeted sequencing.

Exclusion criteria for genotyping experiment	***n***
Concordant replicate - exclude lower call rate	116
Cryptic Duplicate	7
Extreme heterozygous	34
Call rate (<95%)	8
Male	1
Non-European	114
Phenotype data excluded	177
Relative pairs with different status	9
Relative pairs, exclude lower call rate	39
Unclear whether consented when data released in Jan 2012	69
Study duplicates with KARBAC sample	4
Genotype not received	12

eMETHODS

Details on targeted sequencing methodology used by the University of Cambridge (Fluidigm Access Array method)

Targeted sequencing

Target-enriched sequencing libraries of germline DNA from 5,122 breast cancer patients were prepared at the Centre for Cancer Genetic Epidemiology (University of Cambridge). Data used in this study were part of a larger effort that included samples from other cohorts, as well as coding sequences and intron/exon boundaries for a total of 31 known or suspected breast cancer susceptibility genes, including *BRCA1* and *BRCA2*. Assay design was conducted as previously described [2]. See e**Table 2** (**Data Supplement 2**) for primer sequences and amplicon details.

Briefly, target sequence enrichment was performed using 48.48 Fluidigm Access Arrays according to the manufacturer's protocol (Fluidigm, South San Francisco, California, USA). Fluidigm D3 assay design software was used to select primer pairs, which were multiplexed into pools selected for GC content and avoidance of off-target primer-primer and primer-product complementarity. Target sequences were amplified with Illumina sequencing adaptors and one of 1,536 unique sample barcodes (supplied by Fluidigm, South San Francisco, California, USA). Robotic liquid handling and barcode plate identification were used in all steps of the library preparation process. Each library of amplicons (e**Table 2**, **Data Supplement 2**) for 1,536 samples was quantified with the KAPA Library Quantification Kit (KapaBiosystems, Boston, Massachusetts, USA) and then sequenced on the Illumina Hi-Seq 2500 instrument using v4 chemistry, according to the manufacturer's protocol (Illumina, San Diego, California, USA). Each library was sequenced 2-3 times to provide sufficient coverage.

Sequence data processing and quality control

Raw data in *FASTQ* format was received from the University of Cambridge. Paired-end sequencing reads were aligned to the human genome reference sequence (hg19) using Burrows-Wheeler Aligner (version 0.7.12 [3]). Aligned reads in SAM format were converted to BAM format and subsequently merged for each sample using SAMtools (version 1.1 [4]). Read groups were assigned using Picard (version 1.119; http://broadinstitute.github.io/picard). Genome Analysis Toolkit (GATK version 3.7.0; https://software.broadinstitute.org/gatk/) was used for local insertion/deletion (indel) realignment and base quality score recalibration, variant calling, SNP and indel parsing and for deriving quality and depth metrics [5]. The mean read depth across the coding sequences of *BRCA1* and *BRCA2* was 792.2 (standard deviation: 587.4) and 631 (standard deviation: 516), respectively. More than 90% of targeted bases had more than 15x coverage (94.8 [15.9] and 92.5 [20.4] for *BRCA1* and *BRCA2*, respectively).

Genetic variants were called with Unified Genotyper using the default parameters except –mindelFrac 0.05. SNPs and indels with low variant confidence/quality by depth (QD<2) and low approximate read depth (DP<10) were removed. Filter-based annotation of variants were performed using ANNOVAR [6]. A total of 5,099 samples with valid variant calls were included in the final analytical dataset.

Details on targeted sequencing methodology used by the Department of Oncology, Lund University (modified SureSelect hybrid selection method)

The clinical mutation screening was performed using the most sensitive methods available for comprehensive detection of all classes of genetic variants known to affect *BRCA1* and *BRCA2*. Targeted sequencing libraries were prepared using a modified SureSelect hybrid selection method and a custom panel targeting 64 genes including complete *BRCA1* and *BRCA2* loci (exons and introns) and 100kb up- and downstream. Specificity was ensured by confirming all variants with Sanger sequencing on an independent DNA extraction from the patient blood sample. Paired-end sequencing of the libraries was performed on a HiSeq 2500 (2x100bp) to an average depth of ~400 reads. Until 2016, this was complemented with multiple ligation-dependent probe amplification (MLPA) for detection of deletions and duplications affecting one or more complete exons. The lab now has validated bioinformatic methods for detecting these variants directly from the sequencing data. Sensitivity estimated using a large collection of positive control samples including all classes of known pathogenic variants is 100%. Before 2010, denaturing high performance liquid chromatography (DHPLC) and MLPA was used. Together, the DHPLC and MLPA have a stated sensitivity of 95%. Many of the samples tested before 2010 have been screened again using the latest methods.

eTable 3. Swedish Breast Cancer Group criteria for recommending *BRCA1/2* testing.

Criterion	**Number meeting criterion**
Three cases of breast cancer in first degree relatives, or second degree relatives thought a male, with at least one diagnosed ≤50y, and/or ovarian cancer (regardless of age)	79
Two cases of breast cancer or ovarian cancer in first degree relatives, or second degree relatives thought a male, with at least one case of breast cancer diagnosed ≤40y, or two cases of ovarian cancer (regardless of age)	113
One case of breast cancer ≤35y	99
One case of triple-negative breast cancer ≤40y	20
One case of male breast cancer	NA
Breast cancer and ovarian cancer in one individual	44
Cases of bilateral breast cancer, prostate cancer, and pancreatic cancer may strengthen the indication for screening of pathogenic variants in *BRCA1* and *BRCA2*, but are not defined in any specific criterion	NA
Total	298

eTable 4. Description of *BRCA1* (NM_007294.3) pathogenic variants.

Exon	cDNA Change	AA Change	Variant Classification	BIC Nomenclature	Note	*n*
2	c.68_69delAG	p.E23fs	frameshift deletion	185_186delAG,185delAG,187delAG	Founder mutation in Ashkenazi Jews [7]	3
5	c.181T>G	p.C61G	nonsynonymous SNV	300T>G	Common mutation in Europe [8]	1
7	c.302-2A>G	-	splice site	-	-	1
11	c.930delG	p.Q310fs	frameshift deletion	1049delG	-	1
11	c.962G>A	p.W321*	stopgain	W321X	-	1
11	c.1082_1092delCAGAGAATCCT	p.S361*	stopgain	1201del11	Founder mutation common in Southern Sweden [9]	5
11	c.1360_1361delAG	p.S454*	stopgain	1479delAG	-	3
11	c.1504_1508delTTAAA	p.L502fs	frameshift deletion	1623_1627delTTAAA	-	1
11	c.1772delT	p.I591fs	frameshift deletion	1891delT	-	1
11	c.1961delA	p.K654fs	frameshift deletion	2080delA	-	1
11	c.2184delA	p.E729fs	frameshift deletion	-	-	1
11	c.2475delC	p.D825fs	frameshift deletion	2594delC	Swedish BRCA1 founder mutation [10]	2
11	c.3048_3052dupTGAGA	p.N1018fs	frameshift insertion	3166insTGAGA, p.Asn1018fs	Founder mutation originating from West Coast of Sweden [8, 11]	8
11	c.3178G>T	p.E1060*	stopgain	E1060X	-	1
11	c.3485delA	p.D1162fs	frameshift deletion	3604delA	Founder mutation in Finland [8]	1
11	c.3607C>T	p.R1203*	stopgain	3726C>T	-	1
11	c.3626delT	p.L1209*	stopgain	3745delT	Founder mutation originating in Northern Sweden [8]	3
11	c.3700_3704delGTAAA	p.V1234fs	frameshift deletion	3819_3823delGTAAA	Frequent mainly in Middle and Eastern Europe and Canada [12]	1
11	c.4035delA	p.E1346fs	frameshift deletion	4154delA	Common mutation in Poland and Latvia [8]	2
13	c.4201C>T	p.Q1401*	stopgain	-	-	1
13	c.4327C>T	p.R1443*	stopgain	4446C>T	-	1
17	c.5030_5033delCTAA	p.T1677fs	frameshift deletion	5149del4,5147del4,5146del4	-	1
18	c.5075-2A>C	-	splice site	IVS17-2A>C	-	1
18	c.5095C>T	p.R1699W	nonsynonymous SNV	5214C>T	-	1
18	c.5123C>A	p.A1708E	nonsynonymous SNV	5242C>A	-	1
19	c.5153-1G>C	-	splice site	IVS18-1G>C	-	2
20	c.5266dupC	p.Q1756fs	frameshift insertion	5382_5383insC,5382insC,5383insC,5384insC,5385insC	Founder mutation in Russia [13]	3
21	c.5278-2A>T	-	splice site	-	-	1

eTable 5. Description of *BRCA2* (NM_000059.3) pathogenic variants.

Exon	cDNA Change	AA Change	Variant Classification	BIC Nomenclature	Note	*n*
10	c.805dupA	p.T269fs	frameshift insertion	1033insA,p.Thr269fs	-	1
10	c.1310_1313delAAGA	p.K437fs	frameshift deletion	1537_1540delAAAG	-	1
10	c.1796_1800delCTTAT	p.S599*	stopgain	2024_2028delCTTAT	-	1
10	c.1813dupA	p.I605fs	frameshift insertion	2041_2042insA	-	1
11	c.2179delT	p.S727fs	frameshift deletion	-	-	1
11	c.2376C>G	p.Y792*	stopgain	-	-	1
11	c.2476G>T	p.E826*	stopgain	-	-	1
11	c.2578delA	p.I860fs	frameshift deletion	-	-	1
11	c.2808_2811delACAA	p.A938fs	frameshift deletion	3036_3039delACAA	-	1
11	c.3157_3163delTTAGATA	p.L1053fs	frameshift deletion	-	-	1
11	c.3283C>T	p.Q1095*	stopgain	-	-	2
11	c.3847_3848delGT	p.V1283fs	frameshift deletion	4075_4076delGT	-	1
11	c.3860delA	p.N1287fs	frameshift deletion	4088delA,4082delA	-	1
11	c.3950delC	p.T1317fs	frameshift deletion	-	-	1
11	c.5073delA	p.K1691fs	frameshift deletion	5301delA	-	3
11	c.5754_5755delTA	p.H1918fs	frameshift deletion	-	-	2
11	c.5823delA	p.V1942fs	frameshift deletion	6051delA	-	1
11	c.5946delT	p.S1982fs	frameshift deletion	6174delT	Founder mutation in Ashkenazi Jews [8]	4
11	c.6444delT	p.I2149fs	frameshift deletion	-	-	1
11	c.6486_6489delACAA	p.K2162fs	frameshift deletion	6714_6717delACAA	-	2
14	c.7097dupT	p.T2367fs	frameshift insertion	-	-	1
14	c.7414_7415delAA	p.K2472fs	frameshift deletion	7642delAA	-	1
15	c.7443delT	p.T2482fs	frameshift deletion	7671delT	-	1
15	c.7480C>T	p.R2494*	stopgain	7708C>T	-	1
15	c.7558C>T	p.R2520*	stopgain	7786C>T	-	1
16	c.7618-1G>A	-	splice site	IVS15-1G>A	-	1
17	c.7974C>G	p.Y2658*	stopgain	Y2658X	-	1
19	c.8332-1G>A	-	splice site	-	-	1
20	c.8513T>G	p.L2838*	stopgain	8741T>G, p.Leu2838X	-	1
22	c.8910G>A	p.W2970*	stopgain	9138G>A (W-X),p.Trp2970X	-	1
23	c.9097delA	p.T3033fs	frameshift deletion	-	-	2
24	c.9118-2A>G	-	splice site	IVS23-2A>G	-	1
25	c.9403delC	p.L3135fs	frameshift deletion	9631delC	-	1

eTable 6. Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of patient characteristics according to *BRCA* status. *Adjusted for age (<50, 50-59, ≥60) and year of diagnosis (2001-2004 and 2005-2008).

Patient characteristic	**Non-*BRCA* (*n*=5,007)**	***BRCA1* (*n*=50)**	***BRCA2* (*n*=42)**	***BRCA1* vs non-BRCA OR (95% CI)***	***BRCA2* vs non-BRCA OR (95% CI)***	***BRCA2* vs BRCA1 OR (95% CI)***
Age at study entry, years (mean, SD)	63.4 (9.9)	54.9 (12.6)	58.6 (9.4)			
Age at diagnosis, years (mean, SD)	58.6 (9.9)	50.3 (12.4)	54.0 (9.5)			
Age at diagnosis, years (unadjusted)						
<50	887 (17.7)	24 (48.0)	13 (31.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
50-59	1666 (33.3)	13 (26.0)	15 (35.7)	**0.29 (0.15 to 0.57)**	0.61 (0.29 to 1.30)	2.13 (0.78 to 5.81)
≥60	2454 (49.0)	13 (26.0)	14 (33.3)	**0.20 (0.10 to 0.39)**	**0.39 (0.18 to 0.83)**	1.99 (0.72 to 5.47)
Year of diagnosis (unadjusted)						
2001-2004	2325 (46.4)	19 (38.0)	19 (45.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
2005-2008	2682 (53.6)	31(62.0)	23 (54.8)	1.41 (0.80 to 2.51)	1.05 (0.57 to 1.93)	0.74 (0.32 to 1.71)
Education						
University	2113 (42.2)	29 (58.0)	21 (50.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Intermediate	1116 (22.3)	9 (18.0)	12 (28.6)	0.60 (0.28 to 1.27)	1.09 (0.53 to 2.23)	1.51 (0.52 to 4.42)
Elementary	753 (15.0)	3 (6.0)	4 (9.5)	0.48 (0.14 to 1.63)	0.66 (0.22 to 1.96)	1.10 (0.20 to 6.02)
Other	961 (19.2)	9 (18.0)	5 (11.9)	1.05 (0.48 to 2.29)	0.63 (0.23 to 1.72)	0.50 (0.13 to 1.89)
Missing	64 (12.8)	0 (0.0)	0 (0.0)			
Age at menarche, years						
<13	1592 (31.8)	17 (34.0)	11 (26.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥13	3263 (65.2)	33 (66.0)	31 (73.8)	1.12 (0.62 to 2.03)	1.52 (0.76 to 3.06)	1.51 (0.58 to 3.89)
Missing	152 (3.0)	0 (0.0)	0 (0.0)			
BMI, kg/m^2						
<25	2644 (52.8)	28 (56.0)	25 (59.5)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥25	2275 (45.4)	22 (44.0)	16 (38.1)	1.03 (0.58 to 1.81)	0.79 (0.42 to 1.49)	0.84 (0.35 to 2.00)
Missing	88 (1.8)	0 (0.0)	1 (2.4)			
Percentage mammographic density						
<25	2362 (47.2)	15 (30.0)	17 (40.5)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥25	1507 (30.1)	20 (40.0)	10 (23.8)	1.34 (0.66 to 2.75)	0.73 (0.32 to 1.65)	0.52 (0.18 to 1.53)
Missing	1138 (22.7)	15 (30.0)	15 (35.7)			
Number of children						
0	814 (16.3)	8 (16.0)	7 (16.7)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
1	887 (17.7)	10 (20.0)	10 (23.8)	1.26 (0.49 to 3.21)	1.37 (0.52 to 3.62)	0.96 (0.24 to 3.85)
2	2145 (42.8)	19 (38.0)	17 (40.5)	0.98 (0.43 to 2.26)	0.96 (0.40 to 2.33)	0.95 (0.27 to 3.31)
≥3	1130 (22.6)	13 (26.0)	8 (19.0)	1.36 (0.56 to 3.31)	0.89 (0.32 to 2.48)	0.64 (0.16 to 2.54)
Missing	31 (0.6)	0 (0.0)	0 (0.0)			
HRT ever						
No	2208 (44.1)	30 (60.0)	29 (69.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	2694 (53.8)	20 (40.0)	11 (26.2)	1.02 (0.53 to 1.94)	**0.36 (0.17 to 0.75)**	0.36 (0.13 to 1.00)
Missing	105 (2.1)	0 (0.0)	2 (4.8)			
Oral contraceptives ever						
No	1285 (25.7)	11 (22.0)	13 (31.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	3663 (73.2)	39 (78.0)	28 (66.7)	0.87 (0.43 to 1.75)	0.58 (0.29 to 1.16)	0.67 (0.26 to 1.75)
Missing	59 (1.1)	0 (0.0)	1 (2.4)			
Ovarian cancer						
No	4971 (99.3)	44 (88.0)	40 (95.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	36 (0.7)	6 (12.0)	2 (4.8)	**28.02 (10.72 to 73.29)**	**8.11 (1.87 to 35.24)**	0.27 (0.05 to 1.50)
Any malignant cancer, not breast						
No	4494 (89.8)	41 (82.0)	38 (90.5)			
Yes	513 (10.2)	9 (18.0)	4 (9.5)	**2.93 (1.37 to 6.27)**	1.12 (0.39 to 3.20)	0.39 (0.10 to 1.44)

Family history of breast cancer						
No	3948 (78.8)	27 (54.0)	28 (66.7)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	916 (18.3)	23 (46.0)	14 (33.3)	**4.00 (2.27 to 7.05)**	**2.23 (1.17 to 4.26)**	0.60 (0.25 to 1.43)
Missing	143 (2.9)	0 (0.0)	0 (0.0)			
Family history of ovarian cancer						
No	4753 (94.9)	38 (76.0)	36 (85.7)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	231 (4.6)	12 (24.0)	6 (14.3)	**7.53 (3.82 to 14.82)**	**3.62 (1.50 to 8.71)**	0.52 (0.17 to 1.61)
Missing	23 (0.5)	0 (0.0)	0 (0.0)			
Breast cancer in mother						
No	4392 (87.7)	29 (58.0)	32 (76.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	579 (11.6)	21 (42.0)	10 (23.8)	5.17 (2.92 to 9.17)	2.29 (1.12 to 4.68)	0.47 (0.18 to 1.20)
Missing	36 (0.7)	0 (0.0)	0 (0.0)			
Age at breast cancer diagnosis in mother						
<50	92 (15.9)	11 (52.4)	4 (40.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥59	446 (77.0)	9 (42.9)	6 (60.0)	0.20 (0.08 to 0.50)	0.37 (0.10 to 1.35)	2.05 (0.39 to 10.67)
Missing	43 (7.4)	1 (4.8)	0 (0.0)			
Ovarian cancer in mother						
No	4822 (96.3)	39 (78.0)	36 (85.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	149 (3.0)	11 (22.0)	6 (14.3)	9.82 (4.85 to 19.89)	5.44 (2.24 to 13.18)	0.61 (0.20 to 1.86)
Missing	36 (0.7)	0 (0.0)	0 (0.0)			
Ovarian cancer in sister						
No	4885 (97.6)	48 (96.0)	42 (100.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	86 (1.7)	2 (4.0)	0 (0.0)	3.23 (0.76 to 13.76)	-	-
Missing	36 (0.7)	0 (0.0)	0 (0.0)			

eTable 7. Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of tumor characteristics according to *BRCA* status. *Adjusted for age (<50, 50-59, ≥60) and year of diagnosis (2001-2004 and 2005-2008).

Tumor characteristic	**Non-*BRCA* (n=5,007) *n* (%)**	***BRCA1* (n=50) *n* (%)**	***BRCA2* (n=42) *n* (%)**	***BRCA1 vs non-BRCA OR (95% CI)****	***BRCA2 vs non-BRCA OR (95% CI)****	***BRCA2 vs BRCA1 OR (95% CI)****
Type of breast cancer						
Invasive	4470 (89.3)	48 (96.0)	42 (100.0)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Non-invasive	522 (10.4)	2 (4.0)	0 (0.0)	0.37 (0.09 to 1.53)	-	-
Missing	15 (0.3)	0 (0.0)	0 (0.0)			
Detection mode						
Screen-detected	1844 (36.8)	5 (10.0)	12 (28.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Interval	768 (15.3)	5 (10.0)	7 (16.7)	2.36 (0.68 to 8.17)	1.39 (0.54 to 3.54)	0.63 (0.12 to 3.20
Clinical cancer in women without previous mammograms	911 (18.2)	8 (16.0)	4 (9.5)	**3.99 (1.26 to 12.66)**	0.76 (0.24 to 2.43)	0.22 (0.04 to 1.08)
Clinical cancer in women who had previous mammograms (i.e. interval >24 months)	1395 (27.9)	31 (62.0)	19 (45.2)	**5.20 (1.78 to 15.15)**	1.77 (0.73 to 4.29)	0.35 (0.08 to 1.49)
Missing	89 (1.8)	1 (2.0)	0 (0.0)			
Estrogen receptor status						
Positive	3637 (72.6)	17 (34.0)	30 (71.4)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Negative	643 (12.8)	30 (60.0)	7 (16.7)	**8.98 (4.90 to 16.46)**	1.23 (0.54 to 2.82)	**0.14 (0.05 to 0.39)**
Missing	727 (14.5)	3 (6.0)	5 (11.9)			
Progesterone receptor status						
Positive	2952 (59.0)	14 (28.0)	24 (57.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Negative	1252 (25.0)	33 (66.0)	13 (31.0)	**6.06 (3.21 to 11.46)**	1.33 (0.67 to 2.63)	**0.23 (0.09 to 0.60)**
Missing	803 (16.0)	3 (6.0)	5 (11.9)			
Grade						
Well-differentiated	578 (11.5)	1 (2.0)	3 (7.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Moderately differentiated	1563 (31.2)	7 (14.0)	16 (38.1)	2.41 (0.30 to 19.66)	1.91 (0.55 to 6.60)	0.80 (0.07 to 9.47)
Poorly differentiated	822 (16.4)	31 (62.0)	9 (21.4)	**17.99 (2.44 to 132.70)**	1.90 (0.51 to 7.10)	0.11 (0.01 to 1.22)
Missing	2044 (40.8)	11 (22.0)	14 (33.3)			
Tumor size (mm)						
<20	3020 (60.3)	27 (54.0)	23 (54.8)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥20	1608 (32.1)	21 (42.0)	19 (45.2)	1.30 (0.73 to 2.32)	1.47 (0.80 to 2.72)	1.16 (0.46 to 2.89)
Missing	379 (7.6)	2 (4.0)	0 (0)			
Nodal involvement						
No	4503 (89.9)	39 (78.0)	32 (76.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	466 (9.3)	11 (22.0)	10 (23.8)	**2.08 (1.04 to 4.14)**	**2.71 (1.31 to 5.62)**	1.27 (0.46 to 3.54)
Missing	38 (0.8)	0 (0.0)	0 (0.0)			
Proliferation level (Ki67)						
Low (<20%)	923 (18.4)	5 (10.0)	11 (26.2)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
High (≥20%)	736 (14.7)	20 (40.0)	7 (16.7)	**4.25 (1.58 to 11.44)**	0.72 (0.28 to 1.88)	**0.18 (0.04 to 0.74)**
Missing	3348 (66.9)	25 (50.0)	24 (57.1)			
Molecular subtypes						
Luminal A	1212 (24.2)	5 (10.0)	15 (35.7)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Luminal B	156 (3.1)	2 (4.0)	1 (2.4)	2.83 (0.54 to 14.77)	0.49 (0.06 to 3.73)	0.19 (0.01 to 2.60)
HER2-enriched	214 (4.3)	1 (2.0)	1 (2.4)	0.93 (0.11 to 8.07)	0.33 (0.04 to 2.52)	0.38 (0.02 to 8.07)
Basal-like	84 (1.7)	17 (34.0)	1 (2.4)	**40.07 (14.26 to 112.59)**	0.84 (0.11 to 6.43)	**0.02 (0.00 to 0.17)**
Missing	3341 (66.7)	25 (50.0)	24 (57.1)			

eTable 8. Frequency, odds ratio (OR) and corresponding 95% confidence intervals (CI) of tumor characteristics among *BRCA* carriers identified versus not identified through selective clinical screening**.** * Adjusted for year of diagnosis (2001-2004, 2005-2008). † Adjusted for year of diagnosis and gene (*BRCA1*, *BRCA2*). ‡ Adjust for year of diagnosis, gene and age at diagnosis (<50, 50-59, ≥60).

Tumor characteristic	Not identified by selective testing (*n*=57) *n* (%)	Identified by selective testing (*n*=35) *n* (%)	OR (95% CI)*	OR (95% CI)†	OR (95% CI)‡
Type of breast cancer					
Invasive	56 (98.2)	34 (97.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Non-invasive	1 (1.8)	1 (2.9)	2.27 (0.13 to 39.73)	1.11 (0.06 to 20.11)	1.44 (0.06 to 37.74)
Detection mode					
Screen-detected	14 (24.6)	3 (8.6)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Interval	8 (14.0)	4 (11.4)	2.56 (0.44 to 14.85)	2.24 (0.34 to 14.73)	1.56 (0.21 to 11.33)
Clinical cancer in women without previous mammograms	10 (17.5)	2 (5.7)	0.79 (0.11 to 5.72)	0.41 (0.05 to 3.37)	0.48 (0.06 to 4.06)
Clinical cancer in women who had previous mammograms	24 (42.1)	26 (74.3)	**5.52 (1.38 to 22.18)**	3.85 (0.88 to 16.87)	1.88 (0.32 to 11.01)
Missing	1 (1.8)	0 (0.0)			
Estrogen receptor					
Positive	34 (59.6)	13 (37.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Negative	19 (33.3)	18 (51.4)	2.48 (0.99 to 6.19)	1.29 (0.45 to 3.68)	0.81 (0.25 to 2.63)
Missing	4 (7.0)	4 (11.4)			
Progesterone receptor					
Positive	25 (43.9)	13 (37.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Negative	27 (47.4)	19 (54.3)	1.30 (0.53 to 3.19)	0.69 (0.24 to 1.97)	0.46 (0.14 to 1.52)
Missing	5 (8.8)	3 (8.6)			
Grade					
Poorly-differentiated	20 (35.1)	20 (57.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Intermediate-differentiated	18 (31.6)	5 (14.3)	**0.28 (0.08 to 0.92)**	0.48 (0.13 to 1.78)	0.67 (0.17 to 2.70)
Well-differentiated	4 (7.0)	0 (0.0)	-		-
Missing	15 (26.3)	10 (28.6)			
Tumor size (mm)					
<20	35 (61.4)	15 (42.9)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
≥20	16 (28.1)	17 (48.6)	**2.48 (1.00 to 6.16)**	**2.91 (1.07 to 7.92)**	2.15 (0.74 to 6.24)
Missing	5 (8.8)	2 (5.7)			
Nodal involvement					
No	45 (78.9)	26 (74.3)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Yes	12 (21.1)	9 (25.7)	1.40 (0.51 to 3.84)	1.53 (0.52 to 4.52)	1.15 (0.36 to 3.67)
Proliferation level (Ki67)					
Low (<20%)	11 (19.3)	5 (14.3)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
High (≥20%)	12 (21.1)	15 (42.9)	2.75 (0.75 to 10.11)	1.55 (0.37 to 6.43)	0.80 (0.16 to 3.96)
Missing	34 (59.6)	15 (42.9)			
Molecular subtypes					
Luminal A	14 (24.6)	6 (17.1)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Luminal B	2 (3.5)	1 (2.9)	1.17 (0.09 to 15.46)	0.65 (0.04 to 9.93)	0.37 (0.02 to 6.64)
HER2-enriched	2 (3.5)	0 (0.0)	-	-	-
Basal-like	5 (8.8)	13 (37.1)	**6.07 (1.49 to 24.76)**	2.54 (0.52 to 12.41)	1.49 (0.25 to 8.76)
Missing	34 (59.6)	15 (42.9)			

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eTable 2. Primer sequences and amplicon details. Partially overlapping amplicons were tiled across the target regions with a maximum amplicon length (forward and reverse primer length plus intervening unique sequence) of 200-bp. Primers were designed with melting temperature range 59.0-61.0 ℃. Each primer included an orientation-specific tail sequence for subsequent ligation of adapter and barcode sequences.

Gene/Chr	Assay Name	Chr	Start	End	Forward primer	Reverse primer	Total amplicon length	GC %	Amplicon	Flag
BRCA1	BRCA1_3_UTR__exon_24__1	17	41196256	41196454	ACACTGACGACATGGTTCTACAgtgaAAAGGCTCTGAGAAAGTCG	TACGGTAGCAGAGACTTGGTCTGGACTGTTTATAGCTGTTGGAAGGA	199	45	gtgaAAAGGCTCTGAGAAAGTCGGCTGGCCTAAGTCTCAAGAACAGTCATTCATGGTGGAAGTGTTTGCTACCAAGTTTATTTGCAGTGTTAACAGCACAACATTTACAAAACGTATTTTGTACAATCAAGTCTTCACTGCCCTTGCACACTGGGGGGGGCTAGGGAAGACCTAGTCCTTCCAACAGCTATAAACAGTCC	One primer sits in the repeat region
BRCA1	BRCA1_3_UTR__exon_24__2	17	41196303	41196500	ACACTGACGACATGGTTCTACACATTCATGGTGGAAGTGTTTGCT	TACGGTAGCAGAGACTTGGTCTTGCTTGCTGAAGGAAGAAAAAGTG	198	41	CATTCATGGTGGAAGTGTTTGCTACCAAGTTTATTTGCAGTGTTAACAGCACAACATTTACAAAACGTATTTTGTACAATCAAGTCTTCACTGCCCTTGCACACTGGGGGGGCTAGGGAAGACCTAGTCCTTCCAACAGCTATAAACAGTCCTGGATAATGGGTTTATGAGACCTAGTCCTTCCAACAGCTATAAACAGTCCTGGATAATGGGTTTATG	
BRCA1	BRCA1_3UTRB_3	17	41196422	41196600	ACACTGACGACATGGTTCTACAAGACCTAGTCCTTCCAACAGCTA	TACGGTAGCAGAGACTTGGTCTAAATGACAGATCCCACCAGGAAG	179	39	AAAAACACTTTTTCTTCCTTCAGCAAGCAAAATTATTTATGAAGCTGTATGGTTTCAGCAACAGGGAGCAAAGGAAAAAAATCACCTCAAAGAAAGCAACAGCTTCCTTCCTGGTGGGATCTGTCATTT	
BRCA1	BRCA1_3UTRB_4	17	41196516	41196686	ACACTGACGACATGGTTCTACACTGTATGGTTTCAGCAACAGGGA	TACGGTAGCAGAGACTTGGTCTAGTAAAATGTTTATTGTTGTAGCTCTGG	171	36	CTGTATGGTTTCAGCAACAGGGAGCAAAGGAAAAAAATCACCTCAAAGAAAGCAACAGCTTCCTTCCTGGTGGGATCTGTCATTTATTCATGCCAGAGGTCTTATATTTTAAGAGGAATGGATTATATACCAGAGCTACAACAATAAACATTTTACT	
BRCA1	BRCA1_3_UTR__exon_24__5	17	41196609	41196779	ACACTGACGACATGGTTCTACATGAAATATTCATGCCAGAGGTCTT	TACGGTAGCAGAGACTTGGTCTTTTGCTAGATTTCTAAAGAATGTGTTCTAA	171	31	TGAAATATTCATGCCAGAGGTCTTATATTTTAAGAGGAATGGATTATATACCAGAGCTACAACAATAAACATTTTACTTATTACTAATGAGGAATTAGAAGACTGTCTTTGGAAACCGGTTCTTGAAAATCTTCTGCTGTTTTAGAACACATTCTTTAGAAATCTAGCAAA	
BRCA1	BRCA1_3_UTR__exon_24__6	17	41196796	41196982	ACACTGACGACATGGTTCTACAAGAAATCTCTTCTAGTTTCATTTTCCTTT	TACGGTAGCAGAGACTTGGTCTCGGTCATGGTGGTGGACA	187	49	AGAAATCTCTTCTAGtttcattttccttttttttttttttttttgagccacagtctcactgtcacccaggctggagtgccgtggtatgatcttggctcactgcaacctccacctcccgggctgaagtgattctcctgcctagccacctgagtagctgggattacaggtgtccaccaccatgaccg	Two primers sits in the repeat region
BRCA1	BRCA1_3_UTR__exon_24__7	17	41196962	41197133	ACACTGACGACATGGTTCTACAAGGTGTCCACCACCATGA	TACGGTAGCAGAGACTTGGTCTAAGGAAACTTGAAACCTGGGCAT	172	52	aggtgtccaccaccatgaccggctaatttctgtatttttagtagagatgggggtttcaccatgttggccaggctggtttcgaactcctgacctccagtgatctgcccaccttggcctcccaaagtgctgggattacaggcgtgagccaccatgcccagGTTTCAAGTTTCCTTT	Two primers sits in the repeat region
BRCA1	BRCA1_3_UTR__exon_24__8	17	41197109	41197273	ACACTGACGACATGGTTCTACAccatgcccagGTTTCAAGTTT	TACGGTAGCAGAGACTTGGTCTGCAGAGAGTCAGACCCTTCAAT	165	45	ccatgcccagGTTTCAAGTTTCCTTTTCATTTCTAATACCTGCCTCAGAATTTCCTCCCCAATGTTCCACTCCAACATTTGAGAACTGCCCAAGGACTATTCTGACTTTAAGTCACATAATCGATCCCAAGCACTCTCCTTCCATTGAAGGGTCTGACTCTCTGC	One primer sits in the repeat region
BRCA1	BRCA1_3_UTR__exon_24__9	17	41197192	41197381	ACACTGACGACATGGTTCTACAAACTGCCCAAGGACTATTCTGAC	TACGGTAGCAGAGACTTGGTCTTCTATTCAGGCTGTTGTTGGCTT	190	46	AACTGCCCAAGGACTATTCTGACTTTAAGTCACATAATCGATCCCAAGCACTCTCCTTCCATTGAAGGGTCTGACTCTCTTCCAGTTTAGAGAAGTAAACTTAGGGAAACCAGCTATTCTCTTGAGGCCAAGCCACTCTGTGCTTCCAGCCCTAAGCCAACAACAGCCTGAATAGA	
BRCA1	BRCA1_3_UTR__exon_24__10	17	41197309	41197497	ACACTGACGACATGGTTCTACAGGGAAACCAGCTATTCTCTTGAGG	TACGGTAGCAGAGACTTGGTCTGGAAATCTGCCATGAGCACAAAA	189	41	GGGAAACCAGCTATTCTCTTGAGGCCAAGCCACTCTGTGCTTCCAGCCCTAAGCCAACAACAGCCTGAATAGAAAGAATAGGGCTGATAAATAATGAATCAGCATCTTGCTCAATTGGTGGCGTTTAAATGGTTTTAAAATCTTCTCAGGTGAAAAATTACCATAATTTTGTGCTCATGGCAGATTTCC	
BRCA1	BRCA1_3_UTR__exon_24__11	17	41197360	41197558	ACACTGACGACATGGTTCTACAAGCCAACAACAGCCTGAATAGAA	TACGGTAGCAGAGACTTGGTCTCTGAAAAGGACTTCTGGCTATGC	199	39	AGCCAACAACAGCCTGAATAGAAAGAATAGGGCTGATAAATAATGAATCAGCATCTTGCTCAATTGGTGGCGTTTAAATGGTTTTAAAATCTTCTCAGGTGAAAAATTACCATAATTTTGTGCTCATGGCAGATTTCCAAGGGAGACTTCAAGCAGAAAATCTTTAAGGGACCCTTGCAGAGTTTCCAAGGGAGACTTCAAGCAGAAAATCTTTAAGGGACCCTTG	
BRCA1	BRCA1_3_UTR__exon_24__12	17	41197488	41197682	ACACTGACGACATGGTTCTACAGCAGATTTCCAAGGGAGACTTCA	TACGGTAGCAGAGACTTGGTCTACAGGTACAGAGCCACAGGA	195	48	CATAGCCAGAAGTCCTTTTCAGGCTGATGTACATAAAATATTTAGTAGCCAGGACAGTAGAAGGACTGAAGAGTGAGAGGAGCTCCCAGGGCCTGGAAAGGCCACTTTGTAAGCTCATTCTTGGGGTCCTGTGGCTCTGTACCTGTTAGCCAGGACAGTAGAAGGACTGAAGAGTGAGAGGAGCTCCCAGGGCCTGGAAAGGCCACTTTGTAAGCTCATTCTTGGGGTCCTGTGGCTCTGTAC	
BRCA1	BRCA1_3UTRA_3	17	41197582	41197779	ACACTGACGACATGGTTCTACATAGCCAGGACAGTAGAAGGACTG	TACGGTAGCAGAGACTTGGTCTGTGGGTGTTGGACAGTGTAGC	198	57	CTGTGGCTGGCTGCAGTCAGTAGTGGCTGTGGGGGATCTGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACACTGTCCAACACCCAC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_1	17	41197714	41197895	ACACTGACGACATGGTTCTACAATCTGGGGTATCAGGTAGGTGTC	TACGGTAGCAGAGACTTGGTCTCCTGGAGTCGATTGATTAGAGCC	182	52	ATCTGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTGCCTCACACATCTGCCCAATTGCTGGAGACAGAGAACACAAGCAGAGATTAGTGTCAATTCATTCTCCTGGACTAGGCTCTAATCAATCGACTCCAGG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_2	17	41199563	41199750	ACACTGACGACATGGTTCTACATGCCAAGAACTGTGCTACTCAAG	TACGGTAGCAGAGACTTGGTCTTTGAATGCTCTTTCCTTCCTGGG	188	51	tgccaagaactgtgctactcaagcaccaggtaatgagtgataaaccaaacccatgcaaaagGACCCCATATAGCACAGGTACATGCAGGCACCTTACCATGGAAGCCATTGTCCTCTGTCCAGGCATCTGGCTGCACAACCACAATTGGGTGGACACCCTGGATCCCCAGGAAGGAAAGAGCATTCAA	One primer sits in the repeat region
BRCA1	BRCA1_3	17	41201071	41201269	ACACTGACGACATGGTTCTACAGGTGCCAGTCTTGCTCACAG	TACGGTAGCAGAGACTTGGTCTGGCCTGGGTTAAGTATGCAGAT	199	47	GGTGCCAGTCTTGCTCACAGGAGAGAATATTGTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGACATTTAGATGTAAAATCACTGCAGTAATCTGCATACTTAACCCAGGCC	

BRCA1	BRCA1_4	17	41202996	41203184	ACACTGACGACATGGTTCTACACCCATCGTGGGATCTTGCTTAT	TACGGTAGCAGAGACTTGGTCTTTTTCCTTCTCTCCATTCCCCTG	189	51	CCCATCGTGGGATCTTGCTTATAATACTCCACTATGTAAGACAAAGGCTGGTGCTGGAACTCTGGGGTTCTCCCAGGCTCTTACCTGTGGGCATGTTGGTGAAGGGCCCATAGCAACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAGGAAGAGAGAGGGACAGGGGAATGGAGAGAAGGAAAA
BRCA1	BRCA1_5	17	41208999	41209195	ACACTGACGACATGGTTCTACACTCTGCAAAGGGGAGTGGAATAC	TACGGTAGCAGAGACTTGGTCTTCTCTTTCTCTTATCCTGATGGGT	197	46	CTCTGCAAAGGGGAGTGGAATACAGAGTGGTGGGGTGAGATTTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGGGATTCTCTTGCTCGCTTTTGGACCTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGACTTCAAAATCATGCTGAAAGAAACCAAACACAACCCATCAGGATAAGAGAAAGAGA
BRCA1	BRCA1_6	17	41215258	41215442	ACACTGACGACATGGTTCTACAGAAAGTGGTGCATTGATGGAAGG	TACGGTAGCAGAGACTTGGTCTAAGAGCACGTTCTTCTGCTGTAT	185	36	GAAAGTGGTGCATTGATGGAAGGAAGCAAATACATTTTTAACTATATGACTGAATGAATATCTCTGGTTAGTTTGTAACATCAAGTACTTACCTCATTCAGCATTTTTCTTTCTTTAATAGACTGGGTCACCCCTAAAGAGATCATAGAAAAGACAGGTTACATACAGCAGAAGAACGTGCTCTT
BRCA1	BRCA1_7	17	41215830	41216019	ACACTGACGACATGGTTCTACAGGTGTAAAAATGCAATTCTGAGGTGT	TACGGTAGCAGAGACTTGGTCTTCCTGATTTTGTTTTCAACTTCTAATCC	190	37	GGTGTAAAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACCCATTTTCCTCCCGCAATTCCTAGAAAATATTTCAGTGTCCGTTCACACACAAACTCAGCATCTGCAGAATGAAAAACACTCAAAGGATTAGAAGTTGAAAACAAAATCAGGA
BRCA1	BRCA1_8	17	41219582	41219777	ACACTGACGACATGGTTCTACATATGCAGCAGATGCAAGGTATTC	TACGGTAGCAGAGACTTGGTCTAACTAGTATTCTGAGCTGTGTGC	196	35	TATGCAGCAGATGCAAGGTATTCTGTAAAGGTTCTTGGTATACCTGTTTTCATAACAACATGAGTAGTCTCTTCAGTAATTAGATTAGTTAAAGTGATGTGGTGTTTTCTGGCAAACTTGTACACGAGCATCTGAAATTAAATCAAATATTCCATTATCATGAGTTACCTCTAGCACACAGCTCAGAATACTAGTT
BRCA1	BRCA1_Intron_16_1	17	41220845	41221039	ACACTGACGACATGGTTCTACACGTAAGAAGGCTTAGAAGGGGTTC	TACGGTAGCAGAGACTTGGTCTTGGCTAGTAAATGATGGCCCTTG	195	37	CGTAAGAAGGCTTAGAAGGGGTTCATGTTCTTCCCCAAAGAAATTTAGAGTCCTCTAGCTATTATCTATCAACCAAATAAAAATCAATAGGCAGCAAAAGAAATTAACCAGATCAATTATGGGCACAGTTGACCTAGCTGGTAGGTATT
BRCA1	BRCA1_Intron_16_2	17	41220960	41221131	ACACTGACGACATGGTTCTACAATTATGGGCACAGTTGACCTAGC	TACGGTAGCAGAGACTTGGTCTAGTATGGAGTGAGGCAACATGAA	172	44	GTCTGATAAATAACTTTGTTTACCAAGGGCCATCATTTACTAGCCAATTATGGGCACAGTTGACCTAGCTGGTAGGTATTGTCTGATAAATAACTTTGTTTACCAAGGGCCATCATTTACTAGCCACAGTATTTACGTGTTGCACAATACTGCCATGAAGGTCAGGCCATCTTTCTTTTCATGTTGCCTCACTCCATACT
BRCA1	BRCA1_Intron_16_3	17	41221006	41221202	ACACTGACGACATGGTTCTACAACTTTGTTTACCAAGGGCCATCA	TACGGTAGCAGAGACTTGGTCTCGGAGGGTGGTAGCAAAAGG	197	49	ACTTTGTTTACCAAGGGCCATCATTTACTAGCCATAGCCACAGCCACTCACACCAGTATTTACGTGTTGCACAATACTGCCATGAAGGTCAGGCCATCTTTCTTTCATGTTGCCTCACTCCATACTGCCACAGGGCACTGAAAAAAGGCAGGCTAGAGAAGCTAATGACATCCTCCCCCTTTTGCTACCAGGCTCTGAAACTGTTCAGTTAGAAGAGCAATGCTGAACTGCTGAA
BRCA1	BRCA1_Intron_16_4	17	41221097	41221291	ACACTGACGACATGGTTCTACAGGCCATCTTTCTTTCATGTTGCC	TACGGTAGCAGAGACTTGGTCTTTCAGCAGTTCAGCATTGCTCTT	195	47	AAAAAAGGCAGGCTAGAGAAGCTAATGACATCCTCCCCCTTTTGCTACCACCCTCCGCCAGGATCATTAGCAATTCTGAACTGATTAATTGCTGAAATCCCAGCCTTGAAACTGTTCAGTTAGAAGAGCAATGCTGAACTGCTGAAAACTCTTTCCAGAATGTTGTTAAGTCTTAGTCATTAGGGAGATACATATG
BRCA1	BRCA1_9	17	41222884	41223082	ACACTGACGACATGGTTCTACAAACTCTTTCCAGAATGTTGTTAAGTC	TACGGTAGCAGAGACTTGGTCTGCTCATACTACTGATACTGCTGGG	199	43	GATACACTCACAAATTCTTCTGGGGTCAGGCCAGACACCACCATGGACATTCTTTTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_10	17	41222991	41223181	ACACTGACGACATGGTTCTACATTGACCCTTTCTGTTGAAGCTGT	TACGGTAGCAGAGACTTGGTCTGCCCCAGAGTCAGCTCGT	191	48	TTCTTCCATTGCATTATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAGAGGTTGAAGATGGTATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAGAGGTTGAAGATGGTAT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_11	17	41223105	41223287	ACACTGACGACATGGTTCTACATCTGCAACTTTCAATTGGGGAAC	TACGGTAGCAGAGACTTGGTCTTGTGTAAATTAAACTTCTCCCATTCCT	183	46	GTTGCCAACACGAGCTGACTCTGGGGCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATTCCAGATTCCAGGTAAGGGGTTCCCCTCTGAAAGGAATGGGAGAAGTTTAATTTACACA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_12	17	41226290	41226486	ACACTGACGACATGGTTCTACAATGTAGGATTCAGAGTAAAATCAAAGTG	TACGGTAGCAGAGACTTGGTCTTGCTCTGGGAGTCTTCAGAATAGA	197	43	ATGTAGGATTCAGAGTAAAATCAAAGTGTTTGTTCCAATACAGCAGATGAAATATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTGGCCCAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTGAAGACTCCCAGAGCA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_13	17	41226396	41226580	ACACTGACGACATGGTTCTACACAGACTCTTCCAGCTGTTGCT	TACGGTAGCAGAGACTTGGTCTCAATTGGTGGCGATGGTTTTCTC	185	45	CAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTGAAGACTCCCAGAGCAACTGTGCATGTACCACCTATCATCTAATGATGGGCATTTAGAAGGGGATGACCTAGAAAGATAAATGGAAGGAGAAAACCATCGCCACCAATTG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_14	17	41228395	41228576	ACACTGACGACATGGTTCTACATGCCTGTATGCAAAAAACTGGAG	TACGGTAGCAGAGACTTGGTCTCCTTTCTGCTGACAAGTTTGAGG	182	35	TGCCTGTATGCAAAAAACTGGAGAAAGTATGGTGAAAAAAATTAACAATCAGAGTTCAATATAAATAAAGATGTCAGATACCACAGCATCTTTACATTGATGTTTCTTACCTTTCCACTCCTGGTTCTTTATTTTTACTGGTAGAACTATCTGCAGACACCTCAAACTTGTCAGCAGAAAGG
BRCA1	BRCA1_15	17	41228496	41228684	ACACTGACGACATGGTTCTACAGTTTCTTACCTTTCCACTCCTGGT	TACGGTAGCAGAGACTTGGTCTTCACTATCAGAACAAAGCAGTAAAGT	189	37	GTTTCTTACCTTTCCACTCCTGGTTCTTTATTTTTACTGGTAGAACTATCTGCAGACACCTCAAACTTGTCAGCAGAAAGGCCTTCTGGATTCTGGCTTATAGGGTATTCACTACTTTTCTGTGAAGTTAATACTGCTTTAAATGGAATGAGAAAACAAATCTACTTTACTGCTTTGTTCTGATAGTGA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_16	17	41231286	41231459	ACACTGACGACATGGTTCTACAGCCAGAACCACCATCTTTCAGTA	TACGGTAGCAGAGACTTGGTCTAGTACCCGTTCCCTTGATGTCTA	174	42	GCCAGAACCACCATCTTTCAGTAATTTGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCACCTGATATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCATGTATATGCGAATCTGTAAGAAAGGTGAAATTGTAGACATCAAGGGAACGGGTACT
BRCA1	BRCA1_Intron_13_1	17	41231398	41231595	ACACTGACGACATGGTTCTACATGGCCATGTATATGCGAATCTGT	TACGGTAGCAGAGACTTGGTCTTCAATACGCACATTAATTCTCTTGGC	198	43	TGGCCATGTATATGCGAATCTGTAAGAAAGGTGAAATTGTAGACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAAAAGTCTACAACGTGACCCAGCATGCTGTTGGCATCGCTGTAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGTGCGTATTGA
BRCA1	BRCA1_Intron_13_2	17	41231492	41231689	ACACTGACGACATGGTTCTACATGGCAAAACTGGAAAAGTCTACA	TACGGTAGCAGAGACTTGGTCTCCACGTACCTTTCTCTTTGGCTT	198	43	TGGCAAAACTGGAAAAGTCTACAACGTGACCCAGCATGCTGTTGGCATCGCTGTAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGTGCGTATTGAGCACATTAAACACTCTAAGAGCCAAGACAGCTTCCTGAAACGC

Assays designed by relax mode and have no off-target hits

BRCA1	BRCA1_Intron_13_3	17	41231596	41231778	ACACTGACGACATGGTTCTACAGCACATTAAACACTCTAAGAGCCAA	TACGGTAGCAGAGACTTGGTCTGGAATAGGTTCCAGCTGCTCA	183	48	GTGAAGGAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACGTGG GCACATTAAACACTCTAAGAGCCAAGACAGCTTCCTGAAACGCGTGAAG GAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACGTGGGTTC AACTGAAGCACCAGCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAAC CAATGGGAAGGAGCCTGAGCAGCTGGAACCTATTCC CAAAGAGAAAGGTACGTGGGTTCAACTGAAGCACCAGCCTGCTCCACC
BRCA1	BRCA1_Intron_13_4	17	41231671	41231869	ACACTGACGACATGGTTCTACACAAAGAGAAAGGTACGTGGGTTC	TACGGTAGCAGAGACTTGGTCTTGTTCTGGTGATAGAATGACTTTTCTT	199	41	CAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCAGCT GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAAAAAA AAAAAGACCTTTGGACTGTAAAAAAAAAGAAAAGTCATTCTATCACCAGAACA
BRCA1	BRCA1_Intron_13_5	17	41231760	41231936	ACACTGACGACATGGTTCTACAAGCAGCTGGAACCTATTCCCTAT	TACGGTAGCAGAGACTTGGTCTACACAAGGCTTAGGTTGGGCTTCAT	177	32	AGCAGCTGGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAA AAAAAAAAAAAAGACCTTTGGACTGTAAAAAAAAAGAAAAGTCATTCTAT CACCAGAACATTTAGCATATAAATTCCTCTTCTTACTACAATGGGCCTCA TGCAATGAAGCAAATAAGATAACTTGT
BRCA1	BRCA1_Intron_13_6	17	41231851	41232048	ACACTGACGACATGGTTCTACATCATTCTATCACCAGAACATTTAGCA	TACGGTAGCAGAGACTTGGTCTCACAAGGCTTAGGTTGGGCTT	198	35	TCATTCTATCACCAGAACATTTAGCATATAAATTCCTCTTCTTACTACAAT GGGCCTCATGCAATGAAGCAAATAAGATAACTTGTTAGAAGTTAACAACT CAATAGAACCTGAAAAACAGAGCAAAACCTTTCTGCTTTTTTTTCTCCTTA ATCCTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTG
BRCA1	BRCA1_Intron_13_7	17	41231905	41232081	ACACTGACGACATGGTTCTACACCTCATGCAATGAAGCAAATAAGAT	TACGGTAGCAGAGACTTGGTCTTTCCTAAACCAGCCAGCAAGTAG	177	37	CCTCATGCAATGAAGCAAATAAGATAACTTGTTAGAAGTTAACAACTCAA TAGAACCTGAAAAACAGAGCAAAACCTTTCTGCTTTTTTTTCTCCTTAATC CTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTGACATGAT GATCTACTTGCTGGCTGGTTTAGGAA
BRCA1	BRCA1_Intron_13_8	17	41232004	41232201	ACACTGACGACATGGTTCTACATCCTTAATTCATTCTCTGAACAGCA	TACGGTAGCAGAGACTTGGTCTTGGCCCATACTTCCTATCCACAA	198	39	TCCTTAATTCATTCTCTGAACAGCAAGCCCAACCTAAGCCTTGTGACATG ATGATCTACTTGCTGGCTGGTTTAGGAAAGTCTAAATGCAGAGATCCAG AGTCCAAGTTTCAGAATATTATTGTAGTTCCTCTTAAATCATTCCCTCATC TAGATGTCTTAACATGTTACATTCTTTGTGGATAGGAAGTATGGGCCA
BRCA1	BRCA1_17	17	41234313	41234511	ACACTGACGACATGGTTCTACAGAGCAAGGATCATAAAATGTTGGAG	TACGGTAGCAGAGACTTGGTCTAGCCAGCCTTCTAACAGCTAC	199	43	GAGCAAGGATCATAAAATGTTGGAGCTAGGTCCTTACTCTTCAGAAGGA GATAAAGGGGAAGGAAAGAATTTTGCTTAAGATATCAGTGTTTGGCCAA CAATACACACCTTTTTCTGATGTGCTTTGTTCTGGATTTCGCAGGTCCTC AAGGGCAGAAGAGTCACTTATGATGGAAGGGTAGCTGTTAGAAGGCTG GCT
BRCA1	BRCA1_18	17	41234442	41234625	ACACTGACGACATGGTTCTACACTGGATTTCGCAGGTCCTCAAG	TACGGTAGCAGAGACTTGGTCTTCATTTTCTTGGTGCCATTTATCGT	184	46	CTGGATTTCGCAGGTCCTCAAGGGCAGAAGAGTCACTTATGATGGAAGG GTAGCTGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTAGT TCAGCCATTTCCTGCTGGAGCTTTATCAGGTTATGTTGCATGGTATCCCT CTGCTTCAAAAACGATAAATGGCACCAAGAAAATGA
BRCA1	BRCA1_Intron_12__region_2__1	17	41236576	41236770	ACACTGACGACATGGTTCTACAACTCTCCGTTTCTTCTTCTGATCC	TACGGTAGCAGAGACTTGGTCTAATGGCATTGCTGCAGACCTT	195	40	ACTCTCCGTTTCTTCTTCTGATCCTTAAAAATGACTTTGCCCTTTACTAAA AACAAGCCATCTTCTTTCTCCTGCTACACTGAGTTCACAATTTTCAGGAG GTTTTTATGACCAGAAAATGTATTCCTAGCTTCACAAAGGTTTCTACTGCT ACTCTAACACTGCTTTGCTGCCAAGGTCTGCAGCAATGCCATT
BRCA1	BRCA1_Intron_12__region_2__2	17	41236708	41236884	ACACTGACGACATGGTTCTACATCACAAAGGTTTCTACTGCTACTCT	TACGGTAGCAGAGACTTGGTCTCCTGTGAAGCATTTTGGTCAGAT	177	46	TCACAAAGGTTTCTACTGCTACTCTAACACTGCTTTGCTGCCAAGGTCTG CAGCAATGCCATTGCCACCACGTGGTACTCGTGAGTAGTTACATCACTG ATCAAACCCTAGCCAAAGTCTTGCCTCAGTCAACCTGGAATGAAAGCAC ATAGATATCTGACCAAAATGCTTCACAGG
BRCA1	BRCA1_Intron_12__region_2__3	17	41236803	41236999	ACACTGACGACATGGTTCTACAACTGATCAAACCCTAGCCAAAGT	TACGGTAGCAGAGACTTGGTCTTTGGGAAACCCAAAGGAAAGTTA	197	40	ACTGATCAAACCCTAGCCAAAGTCTTGCCTCAGTCAACCTGGAATGAAA GCACATAGATATCTGACCAAAATGCTTCACAGGCTGTATTAGTCACTACT GTCACAACCATCACATCTAACCTCTACGTGGCCATTACATAAATCAGAAA AAGTAGTGGGGTAATTATTAATAGATAACTTTCCTTTGGGTTTCCCAA
BRCA1	BRCA1_Intron_12__region_1__1	17	41237464	41237643	ACACTGACGACATGGTTCTACATGCCATTAGGATAAAATTCCTCAACA	TACGGTAGCAGAGACTTGGTCTAAAAGAGGAGTGGCAGCAAGTAA	180	41	TGCCATTAGGATAAAATTCCTCAACATAGCATTCAAAAGGCCCTTTATAC CCTGGTATTATCTCTCATTTCTCCCAACACCCCTCACACAAGTTGTTTTC CTATAACACATGACAACTTTACGTTTCCTGGGAATTCCATGACTCTGTAC CTTTACCTTACTTGCTGCCACTCCTCTTTT
BRCA1	BRCA1_Intron_12__region_1__2	17	41237543	41237725	ACACTGACGACATGGTTCTACACCCCTCACACAAGTTGTTTTCCT	TACGGTAGCAGAGACTTGGTCTTCATATTTCACAACTCCTCCTGGT	183	42	CCCCTCACACAAGTTGTTTTCCTATAACACATGACAACTTTACGTTTCCT GGGAATTCCATGACTCTGTACCTTTACCTTACTTGCTGCCACTCCTCTTT TTCCACTTGGAAAAATTCTCATCTTTCAAGGCCTAGTTTGAATGTCTCCTT AAGTCCCCACCAGGAGGAGTTGTGAAATATGA
BRCA1	BRCA1_Intron_12__region_1__3	17	41237628	41237825	ACACTGACGACATGGTTCTACACTGCCACTCCTCTTTTTCCACT	TACGGTAGCAGAGACTTGGTCTTATACACTCTGCTTCCCTCCAGA	198	46	CTGCCACTCCTCTTTTTCCACTTGGAAAAATTCTCATCTTTCAAGGCCTA GTTTGAATGTCTCCTTAAGTCCCCACCAGGAGGAGTTGTGAAATATGAG AAGTAAGGGCAAGTGGGCAGAATGTGGCTAATTCTAATAAGACTCCTGA AATGTGCAGCAGAGCAGCCGGAACTGGTCTGGAGGGAAGCAGAGTGTA TA
BRCA1	BRCA1_Intron_12__region_1__4	17	41237700	41237896	ACACTGACGACATGGTTCTACACCACCAGGAGGAGTTGTGAAATA	TACGGTAGCAGAGACTTGGTCTATACACATGTTTTATGGGAAGGTTTT	197	41	CCACCAGGAGGAGTTGTGAAATATGAGAAGTAAGGGCAAGTGGGCAGA ATGTGGCTAATTCTAATAAGACTCCTGAAATGTGCAGCAGAGCAGCCGG AACTGGTCTGGAGGGAAGCAGAGTGTATATCTGACCCTTGTTTGTTCAC ATTCATTACATATAAATATATATATAAAACCTTCCCATAAAACATGTGTAT
BRCA1	BRCA1_19	17	41242903	41243101	ACACTGACGACATGGTTCTACACTACTGAATGCAAAGGACACCAC	TACGGTAGCAGAGACTTGGTCTGCAGCGTTTATAGTCTGCTTTTAC	199	45	CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACACACACAC GCTTTTTACCTGAGTGGTTAAAATGTCACTCTGAGAGGATAGCCCTGAG CAGTCTTCAGAGACGCTTGTTTCACTCTCACACCCAGATGCTGCTTCAC CTTAAATAACAAAAACAGAGGTTCAGATGTAAAAGCAGACTATAAACGCT GC
BRCA1	BRCA1_20	17	41243373	41243569	ACACTGACGACATGGTTCTACAATGTGCTCCCCAAAAGCATAAAC	TACGGTAGCAGAGACTTGGTCTCAGTCTGAAAGCCAGGGAGTTG	197	41	ATGTGCTCCCCAAAAGCATAAACATTTAGCTCACTTCTATAAATAGACTG GGGCAAACACAAAAACCTGGTTCCAATACCTAAGTTTGAATCCATGCTTT GCTCTTCTTGATTATTTTCTTCCAAGCCCGTTCCTCTTTCTTCATCATCTG AAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTTCAGACTG

Assays designed by relax mode and have no off-target hits

BRCA1	BRCA1_21	17	41243485	41243674	ACACTGACGACATGGTTCTACATATTTTCTTCCAAGCCCGTTCCT	TACGGTAGCAGAGACTTGGTCTTCTGCTAGCTTGTTTTCTTCACA	190	43	TATTTTCTTCCAAGCCCGTTCCTCTTTCTTCATCATCTGAAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTTCAGACTGATGCCTCATTTGTTTGGAAGAACCAATCAAGAAAGGATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAATTCACTGCACTGTGAAGAAAACAAGCTAGCAGA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_22	17	41243604	41243793	ACACTGACGACATGGTTCTACAGGATCCTGGGTGTTTGTATTTTGC	TACGGTAGCAGAGACTTGGTCTTGTCTAAGAACACAGAGGAGAATTTA	190	39	GGATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAATTCACTGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTTCCTCACTAAGGTGATGTTCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTGTTCTTAGACA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_23	17	41243699	41243897	ACACTGACGACATGGTTCTACAATGTTCCTGAGATGCCTTTGCC	TACGGTAGCAGAGACTTGGTCTTAGTGAGGATGAAGAGCTTCCCT	199	40	ATGTTCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCATTTAAGCTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTGTTCTTAGACAGACACTCGGTAGCAACGGTGCTATGCCTAGTAGACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCATCCTCACTA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_24	17	41243852	41244044	ACACTGACGACATGGTTCTACAACCAAATAACAAGTGTTGGAAGC	TACGGTAGCAGAGACTTGGTCTTGACATTAAGGAAAGTTCTGCTGTT	193	45	ACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_25	17	41243949	41244145	ACACTGACGACATGGTTCTACATGAGCCAAATGTGTATGGGTGAA	TACGGTAGCAGAGACTTGGTCTCAGCCTATGGGAAGTAGTCATGC	197	43	TGAGCCAAATGTGTATGGGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCATTTTCAGCAAAACTAGTATCTTCCTTTATTTCACCATCATCTAACAGGTCATCAGGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCCGCTTTTGCTAAAAACAGCAGAACTTTCCTTAATGTCATTTTCAGCAAAA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_26	17	41244007	41244197	ACACTGACGACATGGTTCTACACGCTTTTGCTAAAAACAGCAGAAC	TACGGTAGCAGAGACTTGGTCTTCAGACTGTTAATACAGATTTCTCTCCA	191	37	CTAGTATCTTCCTTTATTTCACCATCATCTAACAGGTCATCAGGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCTGTATTAACAGTCTGA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_27	17	41244115	41244295	ACACTGACGACATGGTTCTACACCTGAGATGCATGACTACTTCCC	TACGGTAGCAGAGACTTGGTCTAGATTAGGGGTTTTGCAACCTGA	181	36	CCTGAGATGCATGACTACTTCCCATAGGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCTGTATTAACAGTCTGAACTACTTCTTCATATTCTTGCTTTTTTATTTCAGGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCTAGACCTCAGGTTGCAAAACCCCTAATCT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_28	17	41244171	41244361	ACACTGACGACATGGTTCTACAGGAGAGAAATCTGTATTAACAGTCTGAAC	TACGGTAGCAGAGACTTGGTCTTCCAGTGATGAAAACATTCAAGCA	191	37	GGAGAGAAATCTGTATTAACAGTCTGAACTACTTCTTCATATTCTTGCTTTTTTATTTCAGGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTTCATCactgga	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_29	17	41244266	41244448	ACACTGACGACATGGTTCTACAATAGACCTCAGGTTGCAAAACCC	TACGGTAGCAGAGACTTGGTCTAATGTTTTTAAAGAAGCCAGCTCA	183	38	ATAGACCTCAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTTCATCactggaacctatttcattaatactggagcccacttcattagtactggaacctacttcattaataTTGCTTGAGCTGGCTTCTTTTAAAAACATT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_30	17	41244375	41244557	ACACTGACGACATGGTTCTACAATACTGGAGCCCACTTCATTAGT	TACGGTAGCAGAGACTTGGTCTTCTGCTAGAGGAAAACTTTGAGGA	183	37	atactggagcccacttcattagtactggaacctacttcattaataTTGCTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTATTACGGCTAATTGTGCTCACTGTACTTGGAATGTTCTCATTTCCCATTTCTCTTTCAGGTGACATTGAATGTTCCTCAAAGTTTTCCTCTAGCAGA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_31	17	41244473	41244671	ACACTGACGACATGGTTCTACATGTGCTCACTGTACTTGGAATGT	TACGGTAGCAGAGACTTGGTCTAGGCAACGAAACTGGACTCATTA	199	36	TGTGCTCACTGTACTTGGAATGTTCTCATTTCCCATTTCTCTTTCAGGTGACATTGAATGTTCCTCAAAGTTTTAACAAATGACTTGATGGGAAAAAGTGGTGGTATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAATGAGTCCAGTTTCGTTGCCT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_32	17	41244586	41244763	ACACTGACGACATGGTTCTACAACTTGATGGGAAAAAGTGGTGGT	TACGGTAGCAGAGACTTGGTCTTTTCCTGTGGTTGGTCAGAAAGA	178	39	ACTTGATGGGAAAAAGTGGTGGTATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAATGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAAACCTAGAGCCTCCTTTGATACTACATTTGGCATTATCAACTGGCTTATCTTTCTGACCAACCACAGGAAA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_33	17	41244648	41244841	ACACTGACGACATGGTTCTACAGTAATGAGTCCAGTTTCGTTGCC	TACGGTAGCAGAGACTTGGTCTTGTGAACAAAAGGAAGAAAATCAAGGA	194	40	GTAATGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAAACCTAGAGCCTCCTTTGATACTACATTTGGCATTATCAACTGGCTTATCTTTCTGACCAACCACAGGAAAGCCTGCAGTGATATTAACTGTCTGTACAGGCTTGATATTAGACTCATTCTTTCCTTGATTTTCTTCCTTTTGTTCACA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_34	17	41244742	41244940	ACACTGACGACATGGTTCTACACTTTCTGACCAACCACAGGAAAG	TACGGTAGCAGAGACTTGGTCTGCTCCGTTTTCAAATCCAGGAAA	199	41	CTTTCTGACCAACCACAGGAAAGCCTGCAGTGATATTAACTGTCTGTACAGGCTTGATATTAGACTCATTCTTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGACTTTTGGACTTTGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCATTTCCTGGATTTGAAAACGGAGC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_35	17	41244864	41245040	ACACTGACGACATGGTTCTACATGTTTCTTTAAGGACCCAGAGTG	TACGGTAGCAGAGACTTGGTCTAGTTAACCACAGTCGGGAAACAA	177	42	TGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCATTTCCTGGATTTGAAAACGGAGCTTGAATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCATTTCTATGCTTGTTTCCCGACTGTGGTTAACT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_36	17	41244947	41245144	ACACTGACGACATGGTTCTACACTGGCGCTTTGAAACCTTGAAT	TACGGTAGCAGAGACTTGGTCTGTGAGTCAGTGTGCAGCATTTG	198	40	CTGGCGCTTTGAAACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCATTTCTATGCTTGTTTCCCGACTGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGTGTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGACTCAC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_37	17	41245044	41245232	ACACTGACGACATGGTTCTACATGTCCCAATGGATACTTAAAGCC	TACGGTAGCAGAGACTTGGTCTACCTGGTACTGATTATGGCACTC	189	41	TGTCCCAATGGATACTTAAAGCCTTCTGTGTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGACTCACACATTTATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_38	17	41245154	41245339	ACACTGACGACATGGTTCTACATGGTTCTGTTTTTGCCTTCCCTA	TACGGTAGCAGAGACTTGGTCTACAGTTAAAGTGTCTAATAATGCTGAAGA	186	40	TGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTCAGTTTGCAAAACCCTTTCTCCACTTAACATGAGATCTTTGGGGTCTTCAGCATTATTAGACACTTTAACTGT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_39	17	41245246	41245433	ACACTGACGACATGGTTCTACATGCTACTCTCTACAGATCTTTCAGTT	TACGGTAGCAGAGACTTGGTCTACCTGGTTCTTTTACTAAGTGTTCAAA	188	36	TGCTACTCTCTACAGATCTTTCAGTTTGCAAAACCCTTTCTCCACTTAACATGAGATCTTTGGGGTCTTCAGCATTATTAGACACTTTAACTGTTTCTAGTT	Assays designed by relax mode and have no off-target hits

									TCTCTTCTTTTTCTTCTCTTGGAAGGCTAGGATTGACAAATTCTTTAAGTT CACTGGTATTTGAACACTTAGTAAAAGAACCAGGT	
BRCA1	BRCA1_40	17	41245357	41245539	ACACTGACGACATGGTTCTA CATTTCTTCTCTTGGAAGGC TAGGA	TACGGTAGCAGAGACTTGGTCTA AGGTAAAGAACCTGCAACTGGA	183	39	TTTCTTCTCTTGGAAGGCTAGGATTGACAAATTCTTTAAGTTCACTGGTAT TTGAACACTTAGTAAAAGAACCAGGTGCATTTGTTAACTTCAGCTCTGGG AAAGTATCGCTGTCATGTCTTTTACTTGTCTGTTCATTTGGCTTGTTACTC TTCTTGGCTCCAGTTGCAGGTTCTTTACCTT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_41	17	41245455	41245653	ACACTGACGACATGGTTCTA CAGGGAAAGTATCGCTGTCA TGTCT	TACGGTAGCAGAGACTTGGTCTG CCCACCTAATTGTACTGAATTGC	199	41	GGGAAAGTATCGCTGTCATGTCTTTTACTTGTCTGTTCATTTGGCTTGTT ACTCTTCTTGGCTCCAGTTGCAGGTTCTTTACCTTCCATGAGTTGTAGGT TTCTGCTGTGCCTGACTGGCATTTGGTTGTACTTTTTTTTCTTTATCTCTT CACTGCTAGAACAACTATCAATTTGCAATTCAGTACAATTAGGTGGGC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_42	17	41245543	41245737	ACACTGACGACATGGTTCTA CATGAGTTGTAGGTTTCTGC TGTGC	TACGGTAGCAGAGACTTGGTCTA AGCACCTAAAAAGAATAGGCTGA	195	39	TGAGTTGTAGGTTTCTGCTGTGCCTGACTGGCATTTGGTTGTACTTTTTT TTCTTTATCTCTTCACTGCTAGAACAACTATCAATTTGCAATTCAGTACAA TTAGGTGGGCTTAGATTTCTACTGACTACTAGTTCAAGCGCATGAATATG CCTGGTAGAAGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_43	17	41245646	41245835	ACACTGACGACATGGTTCTA CAAGGTGGGCTTAGATTTCT ACTGAC	TACGGTAGCAGAGACTTGGTCTA GAATCACTCGAAAAAGAATCTGC	190	38	AGGTGGGCTTAGATTTCTACTGACTACTAGTTCAAGCGCATGAATATGCC TGGTAGAAGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTTTGAATTG TGGATATTTAATTCGAGTTCCATATTGCTTATACTGCTGCTTATAGGTTCA GCTTTCGTTTTGAAAGCAGATTCTTTTTCGAGTGATTCT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_44	17	41245703	41245894	ACACTGACGACATGGTTCTA CAAGACTTCCTCCTCAGCCT ATTCT	TACGGTAGCAGAGACTTGGTCTG GTCATGAGAATAAAACAAAAGGT GATTCT	192	35	AGACTTCCTCCTCAGCCTATTCTTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTATAGGTTCAGCTTTCGT TTTGAAAGCAGATTCTTTTTCGAGTGATTCTATTGGGTTAGGATTTTTCTC ATTCTGAATAGAATCACCTTTTGTTTTATTCTCATGACC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_45	17	41245824	41245994	ACACTGACGACATGGTTCTA CATCGAGTGATTCTATTGGG TTAGGA	TACGGTAGCAGAGACTTGGTCTC AAGAAAGCAGATTTGGCAGTTCA	171	36	TCGAGTGATTCTATTGGGTTAGGATTTTTCTCATTCTGAATAGAATCACCT TTTGTTTTATTCTCATGACCACTATTAGTAATATTCATCACTTGACCATTCT GCTCCGTTTGGTTAGTTCCCTGATTTATCATTTCAGGAGTCTTTTGAACT GCCAAATCTGCTTTCTTG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_46	17	41245929	41246123	ACACTGACGACATGGTTCTA CATCCGTTTGGTTAGTTCCC TGATTT	TACGGTAGCAGAGACTTGGTCTC CATGTAACTGAAAATCTAATTATA GGAGCA	195	38	TCCGTTTGGTTAGTTCCCTGATTTATCATTTCAGGAGTCTTTTGAACTGC CAAATCTGCTTTCTTGATAAAATCCTCAGGATGAAGGCCTGATGTAGGTC TCCTTTTACGCTTTAATTTATTTGTGAGGGGACGCTCTTGTATTATCTGTG GCTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_47	17	41246014	41246212	ACACTGACGACATGGTTCTA CAGGCCTGATGTAGGTCTCC TTTTA	TACGGTAGCAGAGACTTGGTCTA GAGTTCACTCCAAATCAGTAGAG	199	39	GGCCTGATGTAGGTCTCCTTTTACGCTTTAATTTATTTGTGAGGGGACGC TCTTGTATTATCTGTGGCTCAGTAACAAATGCTCCTATAATTAGATTTTCA GTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCC CAAATATTTTGTCTTCAATATTACTCTCTACTGATTTGGAGTGAACTCT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_48	17	41246138	41246324	ACACTGACGACATGGTTCTA CAGCTTGCCTTCTTCCGATA GGT	TACGGTAGCAGAGACTTGGTCTA GTAGCTGATGTATTGGACGTTCT	187	37	GCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACT CTCTACTGATTTGGAGTGAACTCTTTCACTTTTACATATTAAAGCCTCATG AGGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCAT CTACCTCATTTAGAACGTCCAATACATCAGCTACT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_49	17	41246190	41246388	ACACTGACGACATGGTTCTA CATCTACTGATTTGGAGTGA ACTCTTT	TACGGTAGCAGAGACTTGGTCTC CAGAAGTGATGAACTGTTAGGT	199	39	TCTACTGATTTGGAGTGAACTCTTTCACTTTTACATATTAAAGCCTCATGA GGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCATC TACCTCATTTAGAACGTCCAATACATCAGCTACTTTGGCATTTGATTCAG ACTCCCCATCATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_50	17	41246313	41246488	ACACTGACGACATGGTTCTA CAACATCAGCTACTTTGGCA TTTGA	TACGGTAGCAGAGACTTGGTCTA ATAAGCAGAAACTGCCATGCTC	176	40	ACATCAGCTACTTTGGCATTTGATTCAGACTCCCCATCATGTGAGTCATC AGAACCTAACAGTTCATCACTTCTGGAAAACCACTCATTAACTTTCTGAA TGCTGCTATTTAGTGTTATCCAAGGAACATCTTCAGTATCTCTAGGATTC TCTGAGCATGGCAGTTTCTGCTTATT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_51	17	41246413	41246606	ACACTGACGACATGGTTCTA CATGCTGCTATTTAGTGTTAT CCAAGG	TACGGTAGCAGAGACTTGGTCTA AGGAGCCAACATAACAGATGGG	194	43	TGCTGCTATTTAGTGTTATCCAAGGAACATCTTCAGTATCTCTAGGATTC TCTGAGCATGGCAGTTTCTGCTTATTCCATTCTTTTCTCTCACACAGGGG ATCAGCATTCAGATCTACCTTTTTTTCTGTGCTGGGAGTCCGCCTATCAT TACATGTTTCCTTACTTCCAGCCCATCTGTTATGTTGGCTCCTT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_52	17	41246501	41246699	ACACTGACGACATGGTTCTA CACTCACACAGGGGATCAGC ATTC	TACGGTAGCAGAGACTTGGTCTA CAGCATGAGAACAGCAGTTTATT	199	42	CTCACACAGGGGATCAGCATTCAGATCTACCTTTTTTTCTGTGCTGGGA GTCCGCCTATCATTACATGTTTCCTTACTTCCAGCCCATCTGTTATGTTG GCTCCTTGCTAAGCCAGGCTGTTTGCTTTTATTACAGAATTCAGCCTTTT CTACATTCATTCTGTCTTTAGTGAGTAATAAACTGCTGTTCTCATGCTGT	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_53	17	41246584	41246781	ACACTGACGACATGGTTCTA CACCCATCTGTTATGTTGGC TCCTT	TACGGTAGCAGAGACTTGGTCTG GCATCCAGAAAAGTATCAGGGTA	198	42	CCCATCTGTTATGTTGGCTCCTTGCTAAGCCAGGCTGTTTGCTTTTATTA CAGAATTCAGCCTTTTCTACATTCATTCTGTCTTTAGTGAGTAATAAACTG CTGTTCTCATGCTGTAATGAGCTGGCATGAGTATTTGTGCCACATGGCT CCACATGCAAGTTTGAAACAGAACTACCCTGATACTTTTCTGGATGCC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_54	17	41246695	41246882	ACACTGACGACATGGTTCTA CAGCTGTAATGAGCTGGCAT GAGTA	TACGGTAGCAGAGACTTGGTCTT TCAGCTGCTTGTGAATTTTCTG	188	43	GCTGTAATGAGCTGGCATGAGTATTTGTGCCACATGGCTCCACATGCAA GTTTGAAACAGAACTACCCTGATACTTTTCTGGATGCCTCTCAGCTGCAC GCTTCTCAGTGGTGTTCAAATCATTATTACTGGGTTGATGATGTTCAGTA TTTGTTACATCCGTCTCAGAAAATTCACAAGCAGCTGAA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_55	17	41246761	41246959	ACACTGACGACATGGTTCTA CACCTGATACTTTTCTGGAT GCCTCT	TACGGTAGCAGAGACTTGGTCTC CACCTCCAAGGTGTATGAAGTA	199	37	CCTGATACTTTTCTGGATGCCTCTCAGCTGCACGCTTCTCAGTGGTGTTC AAATCATTATTACTGGGTTGATGATGTTCAGTATTTGTTACATCCGTCTCA GAAAATTCACAAGCAGCTGAAAATATACAAAAATAACAAGGTACTCAAAA ACTGAATTGTCATTAAAAAAATACATACTTCATACACCTTGGAGGTGG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_56	17	41247808	41248006	ACACTGACGACATGGTTCTA CATGTATCTACCCACTCTCTT TTCAGT	TACGGTAGCAGAGACTTGGTCTG GTCATTTGACAGTTCTGCATAC	199	40	TGTATCTACCCACTCTCTTTTCAGTGCCTGTTAAGTTGGCAAACTTTGCC ATTACCCTTTTTTGCAGAATCCAAACTGATTTCATCCCTGGTTCCTTGAG GGGTGATTTGTAACAATTCTTGATCTCCCACACTATAGGGAAAAGACAGA GTCCTAATAAGAAACACTAGTTACATGTATGCAGAACTGTCAAATGACC acaaactgcacatacatccctgaacctaaaataaaagttaaaaTATTTTTAAAAAGAGAGAA	
BRCA1	BRCA1_57	17	41249130	41249324	ACACTGACGACATGGTTCTA CAACAAACTGCACATACATC CCTGA	TACGGTAGCAGAGACTTGGTCTT GGGGGGAAATTTTTTAGGATCTG	195	32	ACATCAATCCTTAATATTAACTAAATAGGAAAATACCAGCTTCATAGACAA AGGTTCTCTTTGACTCACCTGCAATAAGTTGCCTTATTAACGGTATCTTC AGAAGAATCAGATCCTAAAAAATTTCCCCCCA	Assays designed by relax mode and have no off-target hits

BRCA1	BRCA1_58	17	41249255	41249439	ACACTGACGACATGGTTCTACCAACTCACCTGCAATAAGTTGCCTT	TACGGTAGCAGAGACTTGGTCTGCATTGTACCTGCCACAGTAGAT	185	31	ACTCACCTGCAATAAGTTGCCTTATTAACGGTATCTTCAGAAGAATCAGATCCTAAAAAATTTCCCCCCAAAAAATAAATCAATAAAAGTTTTCTTAATTAAAAGGGTTAAAAAAATGTACTTGTTGAAAAACAGATattcaactagaaatatttactgagcatctactgtggcaggtacaatgc	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_59	17	41251674	41251855	ACACTGACGACATGGTTCTACAATTCACTTCCCAAAGCTGCCTAC	TACGGTAGCAGAGACTTGGTCTGTGAGAACTCTGAGGACAAAGCA	182	37	ATTCACTTCCCAAAGCTGCCTACCACAAATACAAATTATGACCAAGATTTTTGGCAAAACTATAAGATAAGGAATCCAGCAATTATTATTAAATACTTAAAAAACCTGAGACCCTTACCCAATTCAATGTAGACAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCAC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_60	17	41251773	41251963	ACACTGACGACATGGTTCTACAAAAAACCTGAGACCCTTACCCAA	TACGGTAGCAGAGACTTGGTCTCTCTTCAGGAGGAAAAGCACAGA	191	45	AAAAACCTGAGACCCTTACCCAATTCAATGTAGACAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCACAGTTCCAAGGTTAGAGAGTTGGACACTGAGACTGGTTTCCTGCTAAACAGTATGGTAAAGAACAGTCAAGCAATTGTTGGCCAGTTCTGTGCTTTTCCTCCTGAAGAG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_61	17	41256105	41256293	ACACTGACGACATGGTTCTACAAGAAGAAGAAGAAGAAAAACAAATGG	TACGGTAGCAGAGACTTGGTCTCCTTGTATTTTACAGATGCAAACAGC	189	35	agaagaagaagaagaagaaAACAAATGGTTTTACCAAGGAAGGATTTTCGGGTTCACTCTGTAGAAGTCTTTTGGCACGGTTTCTGTAGCCCATACTTTGGATGATAGAAACTTCAAAATTATAGCTGTTTGCATCTGTAAAATACAAGG	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_62	17	41256170	41256368	ACACTGACGACATGGTTCTACAAGTCTTTTGGCACGGTTTCTGTA	TACGGTAGCAGAGACTTGGTCTGCATACATAGGGTTTCTCTTGGT	199	33	AGTCTTTTGGCACGGTTTCTGTAGCCCATACTTTGGATGATAGAAACTTCATCTTTTAGATGTTCAGGAGAGTTATTTTCCTTTTTTGCAAAATTATAGCTGTTTGCATCTGTAAAATACAAGGGAAAACATTATGTTTGCAGTTAGAGAAAAATGTATGAATTATAATCAAAGAAACCAAGAGAAACCCTATGTATGC	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_63	17	41256828	41257012	ACACTGACGACATGGTTCTACATTCCTGAGTTTTCATGGACAGCA	TACGGTAGCAGAGACTTGGTCTTCACTTGCTGAGTGTGTTTCTCA	185	38	TTCCTGAGTTTTCATGGACAGCACTTGAGTGTCATTCTTGGGATATTCAACACTTACACTCCAAACCTGTGTCAAGCTGAAAAGCACAAATGATTTTCAATAGCTCTTCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTGAAATTAAATTGTTTGAGAAACACACTCAGCAAGTGA	Assays designed by relax mode and have no off-target hits
BRCA1	BRCA1_64	17	41258420	41258615	ACACTGACGACATGGTTCTACAACTTTTTCCTACTGTGGTTGCTT	TACGGTAGCAGAGACTTGGTCTTTTTGAGTATTCTTTCTACAAAAGGAAGTAAAT	196	31	ACTTTTTCCTACTGTGGTTGCTTCCAACCTAGCATCATTACCAAATTATATACCTTTTGGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTTCTGGTTGAGAAGTTTCAGCATGCAAAATCTATAAATTATAAAGAAAGAAAGAACAATTTAATTTACTTCCTTTTGTAGAAAGAATACTCAAAA	
BRCA1	BRCA1_65	17	41267715	41267905	ACACTGACGACATGGTTCTACATGGAGCCACATAACACATTCAAA	TACGGTAGCAGAGACTTGGTCTACTCAGTCATAACAGCTCAAAGT	191	37	TGGAGCCACATAACACATTCAAACTTACTTGCAAAATATGTGGTCACACTTTGTGGAGACAGGTTCCTTGATCAACTCCAGACTAGCAGGGTAGGGGGGGAGAAAAAGAAAATAAATGAGGCTCaataatttatttaaaaataaaGCTATTCTTAGTGAATAAGTTCAACTTTGAGCTGTTATGACTGAGT	
BRCA1	BRCA1_Intron_2__region_1__1	17	41271145	41271333	ACACTGACGACATGGTTCTACATGTGACAAGAATGTGGTTTTTTCCT	TACGGTAGCAGAGACTTGGTCTTCCACAAGCTTTTCTTGTGATCC	189	42	TGTGACAAGAATGTGGTTTTTTCCTTAAATATTTAACTTTTTAGAAAAGGATCACAAGggccaggtgcggtggctcacgctgtaatcccagcattttgggaggccaaggcgggccagcctgggtgacagagaatccatctcaaaaaaagaaaaaaaaaaaagaaaaGGATCACAAGAAAAGCTTGTGGA	
BRCA1	BRCA1_Intron_2__region_1__2	17	41271314	41271508	ACACTGACGACATGGTTCTACATCACAAGAAAAGCTTGTGGACAG	TACGGTAGCAGAGACTTGGTCTGAAACAGGTTCAGGTAGAGTGGT	195	42	TCACAAGAAAAGCTTGTGGACAGTAACCTTATTGTGAAGGGTTGTAATACAACTCTTGTAATCATGGGGTTTTTGACATAGCACAGGgcagtgaaaagaaaaacaatgaactaagtcaggaggctgggtttctactaccagttgtgtatataagcagagccaccttgggctaaccactctacctgaacctgtttc	One primer sits in the repeat region
BRCA1	BRCA1_Intron_2__region_1__3	17	41271383	41271556	ACACTGACGACATGGTTCTACATTTTTGACATAGCACAGGGCAGT	TACGGTAGCAGAGACTTGGTCTATTCTTGCAATAGCCCAAGGAGT	174	45	TTTTTGACATAGCACAGGgcagtgaaaagaaaaacaatgaactaagtcaggaggctgggtttctactaccagttgtgtatataagcagagccaccttgggctaaccactctacctgaacctgtttccttctcttgccattcaccctgccagactccttgggctattgcaagaata	Two primers sits in the repeat region
BRCA1	BRCA1_Intron_2__region_1__4	17	41271482	41271675	ACACTGACGACATGGTTCTACAGCTAACCACTCTACCTGAACCTG	TACGGTAGCAGAGACTTGGTCTAAAGTCACATTTGGTCCCAGTAA	194	41	gctaaccactctacctgaacctgtttccttctcttgccattcaccctgccagactccttgggctattgcaagaataaaattaaatgctacttgggaaaatgcttcacaacctgagatgacttgggaaaaatgcttcacaacctgagataacttgTACCAACATTGGTATTATTACTGGGACCAAATGTGACTTT	One primer sits in the repeat region
BRCA1	BRCA1_Intron_2__region_1__5	17	41271534	41271710	ACACTGACGACATGGTTCTACAACTCCTTGGGCTATTGCAAGAAT	TACGGTAGCAGAGACTTGGTCTTCAGAGTTTTCTTTGTCAAGGTTGTT	177	36	actccttgggctattgcaagaataaaattaaatgctacttgggaaaatgcttcacaacctgagatgacttgggaaaaatgcttcacaacctgagataacttgTACCAACATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCCATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCTTGACAAAGAAAACTCTGATTGGTTACTAAATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACT	One primer sits in the repeat region
BRCA1	BRCA1_Intron_2__region_1__6	17	41271642	41271822	ACACTGACGACATGGTTCTACACATTGGTATTATTACTGGGACCAAATGT	TACGGTAGCAGAGACTTGGTCTAGTCAGTGGTGAGAATGAAAGCC	181	33	CATTGGTATTATTACTGGGACCAAATGTGACTTTAAAAAGAAAAACAACCTTGACAAAGAAAACTCTGATTGGTTACTAAATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACT	
BRCA1	BRCA1_Intron_2__region_1__7	17	41271721	41271916	ACACTGACGACATGGTTCTACAAATCCCTATTTCTGAGATAAGCTACAT	TACGGTAGCAGAGACTTGGTCTTCGGAGTTTTCATCTGTTCAAAGT	196	31	AATCCCTATTTCTGAGATAAGCTACATTTCAAAGAAATTCTCCGTAAAAGAAAAATTGGATTCAGTTATCATACCAGATGGCTTTCATTCTCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGA	
BRCA1	BRCA1_Intron_2__region_1__8	17	41271811	41272000	ACACTGACGACATGGTTCTACATCACCACTGACTCAATTCTGAAAC	TACGGTAGCAGAGACTTGGTCTTCAGGACCTAGAAGGGGAACATT	190	31	TCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGATATGTAAAAAGGTAATGAATGTTGAAGGAAGACTGTGAAAAGGGAAAAGAAAAAAAATTAAAATGTTCCCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGA	
BRCA1	BRCA1_Intron_2__region_1__9	17	41271942	41272115	ACACTGACGACATGGTTCTACAAGGAAGACTGTGAAAAGGGAAAAGAA	TACGGTAGCAGAGACTTGGTCTTCACTTATCCGTATTGGAAGCTCA	174	31	TCACCACTGACTCAATTCTGAAACAATTATATTTCAGTATGGTAATTATAATCTAAACTATATAAACACACTGTAAACACAAACTTTGAACAGATGAAAACTCCGATATGTAAAAAGGTAATGAATGTTGAAGGAAGACTGTGAAAAGGGAAAAGAAAAAAAATTAAAATGTTCCCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGA	
BRCA1	BRCA1_Intron_2__region_1__10	17	41271985	41272159	ACACTGACGACATGGTTCTACACCCTTCTAGGTCCTGATGAGAGTA	TACGGTAGCAGAGACTTGGTCTGGTGGGTTGTTGTTTTTCAACCT	175	35	CCCTTCTAGGTCCTGATGAGAGTAAATGTTTACTATAAAAATGATTCAAATATTTTAAACACTTTTCAAACCAGGCAATATTTTAGGCCTACTGTATATTTGCATTTTGAGCTTCCAATACGGATAAGTGACTGGAAAAAGCAGCTAGGTTTAGGTTGAAAAACAACAACCCACC	Multiple hits
BRCA1	BRCA1_Intron_2__region_2__1	17	41275655	41275814	ACACTGACGACATGGTTCTACAGCCCTCGGCCTCATCCAT	TACGGTAGCAGAGACTTGGTCTAATCCTGTGGTCCGGGAAAGAC	160	46	gccctcggccTCATCCATGATTTTATTTTGCCATTTCAAGTGATGGAGCTTGTTTTAGAGCTGGAAGAAAAGCCAAAATGCCAGTTAATCTAAACTAGATTCCTGCCCCAGTGCAGAACCAATCAAGACAGAGTCCCTGTCTTTCCCGGACCACAGGATT	One primer sits in the repeat region

BRCA1	BRCA1_Intron_2__region_2__3	17	41275694	41275869	ACACTGACGACATGGTTCTACAGTGATGGAGCTTGTTTTAGAGCTG	TACGGTAGCAGAGACTTGGTCTTGATTCCTTGTTCTCCATCCACT	176	47	GTGATGGAGCTTGTTTTAGAGCTGGAAGAAAAGCCAAAATGCCAGTTAATCTAAACTAGATTCCTGCCCCAGTGCAGAACCAATCAAGACAGAGTCCCTGTCTTTCCCGGACCACAGGATTTGTGTTGAAAAGGAGAGGAGTGGGAGAGGCAGAGTGGATGGAGAACAAGGAATCA
BRCA1	BRCA1_Intron_2__region_2__4	17	41275796	41275973	ACACTGACGACATGGTTCTACATTTCCCGGACCACAGGATTTG	TACGGTAGCAGAGACTTGGTCTACAGAATTGACCTTACATACTAGGGG	178	38	TTTCCCGGACCACAGGATTTGTGTTGAAAAGGAGAGGAGTGGGAGAGGCAGAGTGGATGGAGAACAAGGAATCATTTTCTATATTTTTAAAGTTCTTCAGTTAAGAAAATCAGCAATTACAATAGCCTAATCTTACTAGACATGTCTTTTCTTCCCTAGTATGTAAGGTCAATTCTGT
BRCA1	BRCA1_Intron_2__region_2__5	17	41275844	41276026	ACACTGACGACATGGTTCTACACAGAGTGGATGGAGAACAAGGAA	TACGGTAGCAGAGACTTGGTCTAGCACAAGAGTGTATTAATTTGGGA	183	33	CAGAGTGGATGGAGAACAAGGAATCATTTTCTATATTTTTAAAGTTCTTCAGTTAAGAAAATCAGCAATTACAATAGCCTAATCTTACTAGACATGTCTTTTCTTCCCTAGTATGTAAGGTCAATTCTGTTCATTTGCATAGGAGATAATCATAGGAATCCCAAATTAATACACTCTTGTGCT
BRCA1	BRCA1_66	17	41275974	41276147	ACACTGACGACATGGTTCTACATCATTTGCATAGGAGATAATCATAGGAA	TACGGTAGCAGAGACTTGGTCTTCTAATGTGTTAAAGTTCATTGGAACAG	174	35	TCATTTGCATAGGAGATAATCATAGGAATCCCAAATTAATACACTCTTGTGCTGACTTACCAGATGGGACACTCTAAGATTTTCTGCATAGCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAATCCATTTCTTTCTGTTCCAATGAACTTTAACACATTAGA
BRCA1	BRCA1_5_UTR__exon_1B__1	17	41277107	41277305	ACACTGACGACATGGTTCTACACTTCCCTCGCGACCTACAAAAC	TACGGTAGCAGAGACTTGGTCTCCTCTGCTCTGGGTAAAGGTAGT	199	60	CTTCCCTCGCGACCTACAAACTGCCCCCCTCCCCAGGGTTCACAACGCCTTACGCCTCTCAGGTTCCGCCCCTACCCCCCGTCAAAGAATACCCATCTGTCAGCTTCGGAAATCCACTCTCCCACGCCAGTACCCCAGAGCATCACTTGGGCCCCCTGTCCCTTTCCCGGGACTCTACTACCTTTACCCAGAGCAGAGG
BRCA1	BRCA1_prom1AextF_1	17	41277234	41277419	ACACTGACGACATGGTTCTACACAGTACCCCAGAGCATCACTT	TACGGTAGCAGAGACTTGGTCTACAGATAAATTAAAACTGCGACTGC	186	59	CAGTACCCCAGAGCATCACTTGGGCCCCCTGTCCCTTTCCCGGGACTCTACTACCTTTACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAGGGGCCCAGTTATCTGAGAAACCCCACAGCCTGTCCCCCGTCCAGGAAGTCTCAGCGAGCTCACGCCGCGCAGTCGCAGTTTTAATTTATCTGT
BRCA1	BRCA1_5_UTR__exon_1A__2	17	41277330	41277526	ACACTGACGACATGGTTCTACACCCAGTTATCTGAGAAACCCCAC	TACGGTAGCAGAGACTTGGTCTCTTTCTGTCCCTCCCATCCTCT	197	54	CCCAGTTATCTGAGAAACCCCACAGCCTGTCCCCCGTCCAGGAAGTCTCAGCGAGCTCACGCCGCGCAGTCGCAGTTTTAATTTATCTGTAATTCCCGCGCTTTTCCGTTGCCACGGAAACCAAGGGGCTACCGCTAAGCAGCAGCCTCTCAGAATACGAAATCAAGGTACAATCAGAGGATGGGAGGGACAGAAAG
BRCA1	BRCA1_prom1AextF_3	17	41277442	41277637	ACACTGACGACATGGTTCTACACACGGAAACCAAGGGGCTAC	TACGGTAGCAGAGACTTGGTCTAGGCACTTTATGGCAAACTCAGG	196	53	CACGGAAACCAAGGGGCTACCGCTAAGCAGCAGCCTCTCAGAATACGAAATCAAGGTACAATCAGAGGATGGGAGGGACAGAAAGAGCCAAGCGTCTCTCGGGGCTCTGGATTGGCCACCCAGTCTGCCCCCGGATGACGTAAAGGAAAGAGACGGAAGAGGAAGAATTCTACCTGAGTTTGCCATAAAGTGCCT
BRCA1	BRCA1_prom1AextF_4	17	41277536	41277729	ACACTGACGACATGGTTCTACATCTCTCGGGGCTCTGGATTG	TACGGTAGCAGAGACTTGGTCTACTGCTTTGGACAATAGGTAGCG	194	51	TCTCTCGGGGCTCTGGATTGGCCACCCAGTCTGCCCCCGGATGACGTAAAAGGAAAGAGACGGAAGAGGAAGAATTCTACCTGAGTTTGCCATAAAGTGCCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGGTCAGAATCGCTACCTATTGTCCAAAGCAGT
BRCA1	BRCA1_Promoter_3	17	41277639	41277818	ACACTGACGACATGGTTCTACACCCTCTAGCCTCTACTCTTCCAG	TACGGTAGCAGAGACTTGGTCTCCCCCCAACAATCCTTATTACTT	180	48	CCCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGGTCAGAATCGCTACCTATTGTCCAAAGCAGTCGTAAGAAGAGGTCCCAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATATAAGTAATAAGGATTGTTGGGGGG
BRCA1	BRCA1_Promoter_4	17	41277726	41277921	ACACTGACGACATGGTTCTACACAGTCGTAAGAAGAGGTCCCAAT	TACGGTAGCAGAGACTTGGTCTTGGTATTGGATGTTCCTCTCCAT	196	46	CAGTCGTAAGAAGAGGTCCCAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATATAAGTAATAAGGATTGTTGGGGGGGTGGAGGGGAAATAATTATTTCCAGCATGCGTTGCGGAATGAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCAATACCA
BRCA1	BRCA1_Promoter_5	17	41277847	41278043	ACACTGACGACATGGTTCTACACGTTGCGGAATGAAAGGTCTTC	TACGGTAGCAGAGACTTGGTCTAGGCCTAGTTTCTGCTTTCAAAAT	197	46	CGTTGCGGAATGAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCAATACCAGAGCGGGCACAATTCTCACGGAAATCCAGTGGATAGATTGGAGACCTGTGCGCGCTTGTACTTGTCAACAGTTATGGACTGGAGTGTTATGTTTTCGTATTTTGAAAGCAGAAACTAGGCCTGGAGAGGAACATCCAATACCAGAGCGGGCACAATTCTCACGGAAATCCA
BRCA1	BRCA1_Promoter_6	17	41277901	41278096	ACACTGACGACATGGTTCTACAGGAGAGGAACATCCAATACCAGAG	TACGGTAGCAGAGACTTGGTCTCTGGGGCTGGATGGGAATTG	196	45	GTGGATAGATTGGAGACCTGTGCGCGCTTGTACTTGTCAACAGTTATGGACTGGAGTGTTATGTTTTCGTATTTTGAAAGCAGAAACTAGGCCTTAAAAAGATACGTACAACTCTTTAGGGAGACTACAATTCCCATCCAGCCCCAGGAGTCTGGGGCAAGTAGTCTTGTAAGGTCAGTGGCCTGCGGGGACGCAGTGAGCGCCGAATTTGCCTGGGGCAGGG
BRCA1	BRCA1_Promoter_7	17	41278016	41278210	ACACTGACGACATGGTTCTACATCGTATTTTGAAAGCAGAAACTAGGC	TACGGTAGCAGAGACTTGGTCTGAACTACGAGTGCGCAGACA	195	53	TCGTATTTTGAAAGCAGAAACTAGGCCTTAAAAAGATACGTACAACTCTTTAGGGAGACTACAATTCCCATCCAGCCCCAGGAGTCTGGGGCAAGTAGCTGGGGCAGGGGAAATGCGCTCTGGCCCATGTCTGCGCACTCGTAGTTC
BRCA1	BRCA1_Promoter_8	17	41278126	41278324	ACACTGACGACATGGTTCTACAAGTGGCCTGCGGGGAC	TACGGTAGCAGAGACTTGGTCTTTACCACTTGTCCCTCAAAACGA	199	59	AGTGGCCTGCGGGGACGCAGTGAGCGCCGAATTTGCCTGGGGCAGGGGAAATGCGCTCTGGCCCATGTCTGCGCACTCGTAGTTCCACCCCTCAGCCCCAGTGTTTGTTATTTTTCGGGTTCAGCTTGCTTTTGCCCCGTCTCCGTCGACGCAATCGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGTGGTAA
BRCA1	BRCA1_Promoter_9	17	41278254	41278449	ACACTGACGACATGGTTCTACACTTTTGCCCCCGTCTCCGT	TACGGTAGCAGAGACTTGGTCTGAGGCGGCAATGCAAAGAC	196	56	CTTTTGCCCCGTCTCCGTCGACGCAATCGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGTGGTAAGAGCCAATCTTCTTGGCGAAAACGCGGAGAAACGGGACTAGTTACTGTCTTTGTCCGCCATGTTAGATTCACCCCACAGAGATAGCGGCAGAGCTGGCAGCGGACGGTCTTTGCATTGCCGCCTC
BRCA1	BRCA1_Promoter_10	17	41278347	41278528	ACACTGACGACATGGTTCTACACGCGGAGAAACGGGACTAGTTA	TACGGTAGCAGAGACTTGGTCTCTCCAAACCCTCTTAGTGTGACG	182	59	CGCGGAGAAACGGGACTAGTTACTGTCTTTGTCCGCCATGTTAGATTCACCCCACAGAGATAGCGGCAGAGCTGGCAGCGGACGGTCTTTGCATTGCCGCCTCCCCACAGGGGCGGGAAGCTGGTAAGGAAGCAGCCTGGGTTAGCTAGGGGTGGGGTCACGTCACACTAAGAGGGTTTGGAG

BRCA1_3UTR_Combined	BRCA1_3UTR_Combined_14	17	41196714	41196888	ACACTGACGACATGGTTCTACATCTTTGGAAACCGGTTCTTG	TACGGTAGCAGAGACTTGGTCTAGATCATACCACGGCACTCC	175	35	TCTTTGGAAACCGGTTCTTGAAAATCTTCTGCTGTTTTAGAACACATTCTTTAGAAATCTAGCAAATATATCTCAGACTTTTAGAAATCTCTTCTAGTTTCATTTTCCTTTTTTTTTTTTTTTTTTTTGAGCCACAGTCTCACTGTCACCCAGGCTGGAGTGCCGTGGTATGATCT
BRCA1_3UTR_Combined	BRCA1_3UTR_Combined_15	17	41197039	41197205	ACACTGACGACATGGTTCTACATCGAACTCCTGACCTCCAGT	TACGGTAGCAGAGACTTGGTCTGTCCTTGGGCAGTTCTCAAA	167	51	TCGAACTCCTGACCTCCAGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGCCCAGGTTTCAAGTTTCCTTTTCATTTCTAATACCTGCCTCAGAATTTCCTCCCCAATGTTCCACTCCAACATTTGAGAACTGCCCAAGGAC
BRCA1_Intron_2__region_1_	BRCA1_Intron_2__region_1__11	17	41271259	41271409	ACACTGACGACATGGTTCTACACAGCCTGGGTGACAGAGAAT	TACGGTAGCAGAGACTTGGTCTTTTCACTGCCCTGTGCTATG	151	38	CAGCCTGGGTGACAGAGAATCCATCTCAAAAAAAGAAAAAAAAAAAAGAAAAGGATCACAAGAAAAGCTTGTGGACAGTAACCTTATTGTGAAGGGTTGTAATACAACTCTTGTAATCATGGGGTTTTTGACATAGCACAGGGCAGTGAAA
BRCA1_Intron_2__region_2_	BRCA1_Intron_2__region_2__7	17	41275415	41275564	ACACTGACGACATGGTTCTACATGGAGTTCAGTGGTGCCATA	TACGGTAGCAGAGACTTGGTCTTGAAACCCCCTCTCCACTAA	150	50	TGGAGTTCAGTGGTGCCATATTGGCTCACAGCAACATCTGCCTCCTGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACTACGCCCAGCTAATTTTTGTATTTTTAGTGGAGAGGGGGTTTCA
BRCA1_Intron_2__region_2_	BRCA1_Intron_2__region_2__8	17	41275545	41275700	ACACTGACGACATGGTTCTACATTAGTGGAGAGGGGGTTTCA	TACGGTAGCAGAGACTTGGTCTCCATCACTTGAAATGGCAAA	156	53	TTAGTGGAGAGGGGGTTTCACCATGTTGGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCTACCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATAAGCCACCGCCCTCGGCCTCATCCATGATTTTATTTTGCCATTTCAAGTGATGG
BRCA2	BRCA2_Promoter_1	13	32888507	32888705	ACACTGACGACATGGTTCTACACACCTTCTGGAAGCAGCAA	TACGGTAGCAGAGACTTGGTCTCATCTTTTGCATTCTTAGGATTCGG	199	47	CACCTTCTGGAAGCAGCAAGGCCCCCATGGGAGCAACTCTCACTGAATCCATTTGAAGGTTTTGTAGGTCTTACAACAAACCCTATTCAGCCTTGTATTAGGCATGTTACAGAACCAACGAATTCGGAGATGAAGTCAGGTCTTCCAGTTCAGCCTGCGAGGAAGACAGGTGATCCGAATCCTAAGAATGCAAAAGATG
BRCA2	BRCA2_Promoter_3	13	32888996	32889147	ACACTGACGACATGGTTCTACAaaaagcaaaaGATACTACCAAGCC	TACGGTAGCAGAGACTTGGTCTTTTAGTTCCAGTAGCTGTTCTGC	152	46	aaaagcaaaaGATACTACCAAGCCCTGCGGAGCAAGGTACCTCACACTTCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGGGCTCGGAGGTCTTGAACACCTGCTACCCAATAGCAGAACAGCTACTGGAACTAAA	One primer sits in the repeat region
BRCA2	BRCA2_Promoter_6	13	32889044	32889230	ACACTGACGACATGGTTCTACATCATGAGCGAGTTAAGATGGGTT	TACGGTAGCAGAGACTTGGTCTAAAAGCTTAGAGTGGTCGGTGTG	187	46	TCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGGGCTCGGAGGTCTTGAACACCTGCTACCCAATAGCAGAACAGCTACTGGAACTAAAATCCTCTGATTTCAAATAACAGCCCCGCCCACTACCACTAAGTGAAGTCATCCACAACCACACACCGACCACTCTAAGCTTTT
BRCA2	BRCA2_prom_Stacey_1	13	32889175	32889357	ACACTGACGACATGGTTCTACACCCACTACCACTAAGTGAAGTCAT	TACGGTAGCAGAGACTTGGTCTTTTTGCTCCAGCTCATGTTTGG	183	50	CCCACTACCACTAAGTGAAGTCATCCACAACCACACACCGACCACTCTAAGCTTTTGTAAGATCGGCTCGCTTTGGGGAACAGGTCTTGAGAGAACATCCCTTTTAAGGTCAGAACAAAGGTATTTCATAGGTCCCAGGTCGTGTCCCGAGGGCGCCCACCCAAACATGAGCTGGAGCAAAAA
BRCA2	BRCA2_prom_Stacey_2	13	32889210	32889390	ACACTGACGACATGGTTCTACACCGACCACTCTAAGCTTTTGT	TACGGTAGCAGAGACTTGGTCTCCCTATGCCTACTCCAAGTCCC	181	52	CACCGACCACTCTAAGCTTTTGTAAGATCGGCTCGCTTTGGGGAACAGGTCTTGAGAGAACATCCCTTTTAAGGTCAGAACAAAGGTATTTCATAGGTCCCAGGTCGTGTCCCGAGGGCGCCCACCCAAACATGAGCTGGAGCAAAAAGAGGGATGGGGGACTTGGAGTAGGCATAGGG
BRCA2	BRCA2_Promoter_Combined_7	13	32889335	32889530	ACACTGACGACATGGTTCTACACCAAACATGAGCTGGAGCAAAAA	TACGGTAGCAGAGACTTGGTCTATTTCTCAGTGTGGCGAAAGGAA	196	54	CCAAACATGAGCTGGAGCAAAAAGAAAGGGATGGGGGACTTGGAGTAGGCATAGGGGCGGCCCCTCCAAGCAGGGTGGCCTGGGACTCTTAAGGGTCAGCGAGAAGAGAACACACACTCCAGCTCCCGCTTTATTCGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCCTTTCGCCACACTGAGAAAT
BRCA2	BRCA2_Promoter_10	13	32889458	32889650	ACACTGACGACATGGTTCTACATCCCGCTTTATTCGGTCAGATAC	TACGGTAGCAGAGACTTGGTCTGCCTCTGCCGCCTAGTT	193	62	TCCCGCTTTATTCGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCCTTTCGCCACACTGAGAAATACCCGCAGCGGCCCACCCAGGCCTGACTTCCGGGTGGTGCGTGTGCTGCGTGTCGCGTCACGGCGTCACGTGGCCAGCGCGGGCTTGTGGCGCGAGCTTCTGAAACTAGGCGGCAGAGGC
BRCA2	BRCA2_Promoter_Combined_10	13	32889508	32889703	ACACTGACGACATGGTTCTACATTCCTTTCGCCACACTGAGAAAT	TACGGTAGCAGAGACTTGGTCTCCGCAAAAGACACCCGAGG	196	67	TTCCTTTCGCCACACTGAGAAATACCCGCAGCGGCCCACCCAGGCCTGACTTCCGGGTGGTGCGTGTGCTGCGTGTCGCGTCACGGCGTCACGTGGCCAGCGCGGGCTTGTGGCGCGAGCTTCTGAAACTAGGCGGCAGAGGCGGAGCCGCTGTGGCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGCGG
BRCA2	BRCA2_5_UTR__exon_1__2	13	32889663	32889835	ACACTGACGACATGGTTCTACAGCACTGCTGCGCCTCT	TACGGTAGCAGAGACTTGGTCTCTCGTCCCAACCCACTACCA	173	62	GCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGCGGCGGTGGGTCGCCGCCGGGAGAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTCAGCTTACTCCGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTAGTGGGTTGGGACGAG
BRCA2	BRCA2_prom_Stacey_7	13	32889723	32889921	ACACTGACGACATGGTTCTACAGAAGCGTGAGGGGACAGATTT	TACGGTAGCAGAGACTTGGTCTAGAGACAAAAGGGCAAGAAGCC	199	63	GAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTCAGCTTACTCCGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTAGTGGGTTGGGACGAGCGGCGTCTTCCGCAGTCCCAGTCCAGCGTGGCGGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTTGTCTCT
BRCA2	BRCA2_prom_Stacey_8	13	32889839	32890018	ACACTGACGACATGGTTCTACAGTCTTCCGCAGTCCCAGTC	TACGGTAGCAGAGACTTGGTCTGAAATGGAGACCCAGGGAAGG	180	64	GTCTTCCGCAGTCCCAGTCCAGCGTGGCGGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTTGTCTCTGCCAACCCCCACCCATGCCTGAGAGAAAGGTCCTTGCCCGAAGGCAGATTTTCGCCAAGCAAATTCGAGCCCCGCCCCTTCCCTGGGTCTCCATTTC
BRCA2	BRCA2_1	13	32890522	32890720	ACACTGACGACATGGTTCTACATCCCTGTGTAAGTGCATTTTGGT	TACGGTAGCAGAGACTTGGTCTTTTAGAAAACACTTTCTCGGTGTAAT	199	34	TCCCTGTGTAAGTGCATTTTGGTCTTCTGTTTTGCAGACTTATTTACCAAGCATTGGAGGAATATCGTAGGTAAAAATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGGTATTGACAAATTTTATATAACTTTATAAATTACACCGAGAAAGTGTTTTCTAAAA
BRCA2	BRCA2_2	13	32893174	32893358	ACACTGACGACATGGTTCTACATCACTGGTTAAAACTAAGGTGGGA	TACGGTAGCAGAGACTTGGTCTTAAGATGGTTTCCTTTGTGGAGT	185	32	TCACTGGTTAAAACTAAGGTGGGATTTTTTTTTTAAATAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAAT

								TCTGAACCTGCAGAAGAATCTGAACATAAAAACAACAATTACGAACCAAA CCTATTTAAAACTCCACAAAGGAAACCATCTTA	
BRCA2	BRCA2_3	13	32893249	32893426	ACACTGACGACATGGTTCTA CACTTTCTTCAGAAGCTCCA CCCTA	TACGGTAGCAGAGACTTGGTCTG AGATTGGTACAGCGGCAGAG	178	39	CTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATCTGA ACATAAAAACAACAATTACGAACCAAACCTATTTAAAACTCCACAAAGGA AACCATCTTATAATCAGCTGGCTTCAACTCCAATAATATTCAAAGAGCAA GGGCTGACTCTGCCGCTGTACCAATCTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_4	13	32893336	32893492	ACACTGACGACATGGTTCTA CAACTCCACAAAGGAAACCA TCTTA	TACGGTAGCAGAGACTTGGTCTC TCCCCAGTCTACCATATTGCAT	157	39	ACTCCACAAAGGAAACCATCTTATAATCAGCTGGCTTCAACTCCAATAAT ATTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTCCTGTAAAA GAATTAGATAAATTCAAATTAGACTTAGGTAAGTAATgcaatatggtagactgggg ag	One primer sits in the repeat region
BRCA2	BRCA2_Intron_3_1	13	32897972	32898163	ACACTGACGACATGGTTCTA CAACTTAATGCCCTGGAGAG TCAAA	TACGGTAGCAGAGACTTGGTCTA GACAAAGTGAGTTGCAGACAGTA	192	29	ACTTAATGCCCTGGAGAGTCAAATATAATCTACTCTAATACAGAAAATAG AAATATTGAAAAACTGTAAATTGGATTTCATATTGTTAAAGCCACCTATAG CTTTAGAAACTCTGAACATTATTTTCTTAGAAAATGGATGTGTTCAATAAG AATAGAAATTATGTATTACTGTCTGCAACTCACTTTGTCT	
BRCA2	BRCA2_Intron_3_2	13	32898044	32898221	ACACTGACGACATGGTTCTA CAGGATTTCATATTGTTAAAG CCACCTAT	TACGGTAGCAGAGACTTGGTCTT GTCTGGTATATTAGTCACTCCTG AA	178	30	GGATTTCATATTGTTAAAGCCACCTATAGCTTTAGAAACTCTGAACATTAT TTTCTTAGAAAATGGATGTGTTCAATAAGAATAGAAATTATGTATTACTGT CTGCAACTCACTTTGTCTAATTATATCCAatttattcatccagtcaatatttcaggagtgact aatataccagaca	One primer sits in the repeat region
BRCA2	BRCA2_Intron_3_3	13	32898141	32898311	ACACTGACGACATGGTTCTA CAACTGTCTGCAACTCACTT TGTCT	TACGGTAGCAGAGACTTGGTCTA CACTGTTCTTTTTCCCCCTACT	171	37	ACTGTCTGCAACTCACTTTGTCTAATTATATCCAatttattcatccagtcaatatttcag gagtgactaatataccagacatttttgtagttgctagggatacagtgacaaataagacaaaatctctacctca gattgctcacagcctagtaggggaaaaagaacagtgt	One primer sits in the repeat region
BRCA2	BRCA2_Intron_3_4	13	32898184	32898355	ACACTGACGACATGGTTCTA CATCCAGTCAATATTTCAGG AGTGACTAA	TACGGTAGCAGAGACTTGGTCTT TAAGTGTTTGCCCCCCTATGTG	172	40	tccagtcaatatttcaggagtgactaatataccagacatttttgtagttgctagggatacagtgacaaataag acaaaatctctacctcagattgctcacagcctagtaggggaaaaagaacagtgtatgatcaaactcttca gggaacacataggggggcaaacacttaa	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_3_5	13	32898267	32898457	ACACTGACGACATGGTTCTA CATACCTCAGATTGCTCACA GCCTA	TACGGTAGCAGAGACTTGGTCTG CTGTTTCCCCTTCTTTGCTTTT	191	44	tacctcagattgctcacagcctagtaggggaaaaagaacagtgtatgatcaaactcttcagggaacaca taggggggcaaacacttaatcttaccttagggatcactacagttttctggaggaggtagtttctaaatggaag cctgaaagagttgttccaggtcaagaaaagcaaagaaggggaaacagc	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_3_6	13	32898366	32898559	ACACTGACGACATGGTTCTA CAGGGATCACTACAGTTTTC TGGAGG	TACGGTAGCAGAGACTTGGTCTA ATTTTTATGATGCCATTCTTTTAC AGTC	194	38	gggatcactacagttttctggaggaggtagtttctaaatggaagcctgaaagagttgttccaggtcaagaaa agcaaagaaggggaaacagcttgtacaaagtcctagaggttaaagaaaacattctttcaggatatgcaa atggttgggtatgggtaaaaagtagactgtaaaagaatggCATCATAAAAATT	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_3_7	13	32898426	32898622	ACACTGACGACATGGTTCTA CACAGGTCAAGAAAAGCAAA GAAGGG	TACGGTAGCAGAGACTTGGTCTT TTCTTCATTTTTAATTTTTGTGGG TACAT	197	30	caggtcaagaaaagcaaagaaggggaaacagcttgtacaaagtcctagaggttaaagaaaacattctttt caggatatgcaaatggttgggtatgggtaaaaagtagactgtaaaagaatggCATCATAAAAATT AAGTAAATTGTCAcataaatatatatattttcttatgtacccacaaaaattaaaaaTGAAGAAA	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_3_8	13	32898527	32898716	ACACTGACGACATGGTTCTA CAAGTAGACTGTAAAAGAAT GGCATCA	TACGGTAGCAGAGACTTGGTCTT GACAATATCACTTGTGCTAAAAAC CT	190	27	agtagactgtaaaagaatggCATCATAAAAATTAAGTAAATTGTCAcataaatatatatattttcttatgtacccacaaaaattaaaaaTGAAGAAATTAAGTAAATTGTCACATCATAAAAATT TACTATGGAGTTTGACTTGATCTTGAAAAGTAAGATCTTGAAAGGTTTTTA GCACAAGTGATATTGTCA	One primer sits in the repeat region
BRCA2	BRCA2_5	13	32899149	32899334	ACACTGACGACATGGTTCTA CACCAAAGAATGCAAATTTAT AATCCAGAGT	TACGGTAGCAGAGACTTGGTCTA GCTTCATCATACCTTTCACTAAGA C	186	34	ccaaagaatgcaaatttataatcCAGAGTATATACATTCTCACTGAATTATTGTACTG TTTCAGGAAGGAATGTTCCCAATAGTAGACATAAAAGTCTTCGCACAGTG AAAACTAAAATGGATCAAGCAGATGATGTTTCCTGTCCACTTCTAAATTC TTGTCTTAGTGAAAGGTATGATGAAGCt	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_6	13	32899280	32899435	ACACTGACGACATGGTTCTA CATGATGTTTCCTGTCCACTT CTAAA	TACGGTAGCAGAGACTTGGTCTT CTACCAGGCTCTTAGCCAAAAT	156	28	TGATGTTTCCTGTCCACTTCTAAATTCTTGTCTTAGTGAAAGGTATGATGA AGCtattatattaaaatatttaaatGAAACATTTTCCTACATATATTTGTTCTATAAAG ATGAATCTGATTTTTATGCTAATATTTTGGCTAAGAGCCTGGTAGA	
BRCA2	BRCA2_7	13	32900202	32900400	ACACTGACGACATGGTTCTA CAAAAATAACCTAAGGGATT TGCTTTGT	TACGGTAGCAGAGACTTGGTCTT GAAACAAACTCCCACATACCACT	199	30	AAAATAACCTAAGGGATTTGCTTTGTTTTATTTTAGTCCTGTTGTTCTACA ATGTACACATGTAACACCACAAAGAGATAAGTCAGGTATGATTAAAAACA ATGCTTTTTATTCTTAGAATACTAGAAATGTTAATAAAAATAAAACTTAACA ATTTTCCCCTTTTTTTACCCCCAGTGGTATGTGGGAGTTTGTTTCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_8	13	32900331	32900527	ACACTGACGACATGGTTCTA CATGTTAATAAAAATAAAACT TAACAATTTTCCCCTT	TACGGTAGCAGAGACTTGGTCTT GAGGCAGAATGCTAGGTACAGA	197	33	TGTTAATAAAAATAAAACTTAACAATTTTCCCCTTTTTTTACCCCCAGTGG TATGTGGGAGTTTGTTTCATACACCAAAGTTTGTGAAGGTAAATATTCTA CCTGGTTTATTTTTATGACTTAGTAATTGAGAATTTGACAATAGCGTTATA CCTTTGCCCTGAGATTTACAAATCTGTACCTAGCATTCTGCCTCA	
BRCA2	BRCA2_9	13	32900545	32900728	ACACTGACGACATGGTTCTA CAACGTTAAGTGAAATAAAG AGTGAATGAA	TACGGTAGCAGAGACTTGGTCTG GTGGGTGGTGTAGCTAAAGA	184	37	ACGTTAAGTGAAATAAAGAGTGAATGAAAAAATAATATCCTTAATGATCA GGGCATTTCTATAAAAAATAAACTATTTTCTTTCCTCCCAGGGTCGTCAG ACACCAAAACATATTTCTGAAAGTCTAGGAGCTGAGGTGGATCCTGATAT GTCTTGGTCAAGTTCTTTAGCTACACCACCCACC	
BRCA2	BRCA2_10	13	32900618	32900797	ACACTGACGACATGGTTCTA CATATTTTCTTTCCTCCCAGG GTCGT	TACGGTAGCAGAGACTTGGTCTT CAACCTCATCTGCTCTTTCTTG	180	41	TATTTTCTTTCCTCCCAGGGTCGTCAGACACCAAAACATATTTCTGAAAG TCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTA CACCACCCACCCTTAGTTCTACTGTGCTCATAGGTAATAATAGCAAATGT GTATTTACAAGAAAGAGCAGATGAGGTTGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_11	13	32903475	32903668	ACACTGACGACATGGTTCTA CATGTGTCATGTAATCAAATA GTAGATGTG	TACGGTAGCAGAGACTTGGTCTA GCAATTTCAACAGTCTAATCAATG TC	194	29	TGTGTCATGTAATCAAATAGTAGATGTGCTTTTTGATGTCTGACAAAAAAT AAGTTTTTGCATTCTAGTGATAATATACAATACACATAAATTTTTATCTTAC AGTCAGAAATGAAGAAGCATCTGAAACTGTATTTCCTCATGATACTACTG CTGTAAGTAAATATGACATTGATTAGACTGTTGAAATTGCT	
BRCA2	BRCA2_Intron_8_1	13	32904422	32904620	ACACTGACGACATGGTTCTA CATGTGACAGCAAAACCAGC TCATA	TACGGTAGCAGAGACTTGGTCTG GCCCCAAAGCACAAGTATAATG	199	38	tgtgacagcaaaaccagctcatatgtctttctccttcacaatctcacagatagatttgttcttaccatagatgtcg cagtacaatttttttccttttcctttaagtcgagaactttcactgtttcaattaaaggaagcactttatggcttcttttttgg catatttgaattgccagcatcattatactttgtgctttggggcc	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_8_2	13	32904478	32904657	ACACTGACGACATGGTTCTA CATGTTCTTACCATAGATGTC GCAGT	TACGGTAGCAGAGACTTGGTCTT GCTTGTGTTCAAGTCACCCTTA	180	36	tgttcttaccatagatgtcgcagtacaatttttttccttttcctttaagtcgagaactttcactgtttcaattaaaggaa gcactttatggcttcttttttggcatatttgaattgccagcatcattatactttgtgctttggggccattgttaagtaaaa taagggtgacttgaacacaagca	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_8_3	13	32904600	32904770	ACACTGACGACATGGTTCTA CATTATACTTGTGCTTTGGG GCCAT	TACGGTAGCAGAGACTTGGTCTA CTTGGGACATGAATCATCCCTT	171	43	ttatacttgtgctttggggccattgttaagtaaaataagggtgacttgaacacaagcactgtggtaccacaata gccgatctgataaccaagacaactactaagtgactaataggtgggtaccatatacagcctggatacgctg gacaaagggatgattcatgtcccaagt	Two primers sits in the repeat region

BRCA2	BRCA2_Intron_8_4	13	32904673	32904852	ACACTGACGACATGGTTCTACAAGCCGATCTGATAACCAAGACAA	TACGGTAGCAGAGACTTGGTCTCTTGCACCACTAGGATGTGGAAA	180	43	agccgatctgataaccaagacaactactaagtgactaataggtgggtaccatatacagcctggatacgctggacaaagggatgattcatgtcccaagtgggatggagcaagatggtgcaagttttttttctccatttccattttccttctaagatttccacatcctagtggtgcaag	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_8_5	13	32904749	32904920	ACACTGACGACATGGTTCTACAAGGGATGATTCATGTCCCAAGTG	TACGGTAGCAGAGACTTGGTCTGGAAAATTCCAGAAGTAAGCAATTAGT	172	38	agggatgattcatgtcccaagtgggatggagcaagatggtgcaagttttttttctccatttccattttcctttcctaagatttccacatcctagtggtgcaagatttcatcacactactcaggatgacacacaatttaaaacttactaattgcttacttctggaattttcc	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_8_6	13	32904844	32905015	ACACTGACGACATGGTTCTACATGGTGCAAGATTTCATCACACTA	TACGGTAGCAGAGACTTGGTCTTCAATGCACATATAGTAGTAGTCCC	172	35	tggtgcaagatttcatcacactactcaggatgacacacaatttaaaacttactaattgcttacttctggaattttccattaaaaattttggacctaggttgattgcagataactgaaatcaccaaaagtgaaaccatggataaggggactactACTATATGTGCATTGA	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_8_7	13	32904887	32905077	ACACTGACGACATGGTTCTACAAAAACTTACTAATTGCTTACTTCTGGAAT	TACGGTAGCAGAGACTTGGTCTTGGAAAAATAGCTTTTCACATTCTGC	191	31	aaaacttactaattgcttacttctggaattttccattaaaaattttggacctaggttgattgcagataactgaaatcaccaaaagtgaaaccatggataaggggggactactACTATATGTGCATTGAGAGTTTTTATACTAGTGATTTTAAACTATACTAGTGATTTTAAACTATAATTTTTGCAGAATGTGAAAAGCTATTTTTCCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_12	13	32904990	32905188	ACACTGACGACATGGTTCTACAGGGGACTACTACTATATGTGCATTGA	TACGGTAGCAGAGACTTGGTCTTCAACTAAACAGAGGACTTACCATGA	199	33	ggggactactACTATATGTGCATTGAGAGTTTTTATACTAGTGATTTTAAACTATAATTTTTGCAGAATGTGAAAAGCTATTTTTCCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGCTTCTGTGACAGACAGTGAAAACACAAATCAAAGAAGCTGCAAGTCATGGTAAGTCCTCTGTTTAGTTGAACTACAGGTTTTTTTGTTGTTGTTGTTTTGACTGTGACAGACAGTGAAAACACAAATCAAAGAGAAGCTGCAAGTCATGGTTTTTTTTTTTTGAGGTGGAGTCTTGCTCTGTCACCCGTGATCTCGGTTTACCGCAACCT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_126	13	32905120	32905279	ACACTGACGACATGGTTCTACACTGTGACAGACAGTGAAAACACA	TACGGTAGCAGAGACTTGGTCTAGGTTGCGGTAAACCGAGAT	160	40		
BRCA2	BRCA2_13	13	32906365	32906537	ACACTGACGACATGGTTCTACATGGCTTATAAAATATTAATGTGCTTCTGT	TACGGTAGCAGAGACTTGGTCTAACTATCTTCTTCAGAGGTATCTACAAC	173	32	TGGCTTATAAAATATTAATGTGCTTCTGTTTTATACTTTAACAGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAAGACCACATTGGAAAGTCAATGCCAAATGTCCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_14	13	32906405	32906593	ACACTGACGACATGGTTCTACAACAGGATTTGGAAAAACATCAGGG	TACGGTAGCAGAGACTTGGTCTGCTAGTTCTTACTTTTTGTAGATTTTTGTTCT	189	31	ACAGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAAGACCACATTGGAAAGTCAATGCCAAATGTCCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAAATCTACAAAAAGTAAGAACTAGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_15	13	32906502	32906695	ACACTGACGACATGGTTCTACAATGAAACAGTTGTAGATACCTCTGAA	TACGGTAGCAGAGACTTGGTCTTGGTTCCACTTCAGATACAAATGAGT	194	29	ATGAAACAGTTGTAGATACCTCTGAAGAAGATAGTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAAATCTACAAAAAGTAAGAACTAGCAAGACTAGGAAAAAAATTTTCCATGAAGCAAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_16	13	32906614	32906786	ACACTGACGACATGGTTCTACACCATGAAGCAAACGCTGATGAAT	TACGGTAGCAGAGACTTGGTCTAAGACGGTACAACTTCCTTGGAG	173	36	CCATGAAGCAAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAAAAATACTCATTTGTATCTGAAGTGGAAGTGACAAAAGATTCAAATGTAGCAAATCAGAAGCCCTTTGAGAGTGGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_17	13	32906677	32906859	ACACTGACGACATGGTTCTACATGTATCTGAAGTGGAACCAAATGA	TACGGTAGCAGAGACTTGGTCTTGCAATAGGGGTATTTTCTCCAT	183	42	TGTATCTGAAGTGGAACCAAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGAAGCCCTTTGAGAGTGGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGATGGAGAAAATACCCCTATTGCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_18	13	32906777	32906973	ACACTGACGACATGGTTCTACAGTACCGTCTTTGGCCTGTGAATG	TACGGTAGCAGAGACTTGGTCTGGTAGGCTAGAAATACGTGGCAAA	197	39	GTACCGTCTTTGGCCTGTGAATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGATGGAGAAAATACCCCTATTGCATAATTTCTTCATGTGACCAAAATATTTCAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGAATTCTTTGCCACGTATTTCTAGCCTACC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_19	13	32906851	32907049	ACACTGACGACATGGTTCTACACCTATTGCATATTTCTTCATGTGACC	TACGGTAGCAGAGACTTGGTCTTGTATGAGATTCAAGATGCTGCT	199	34	CCTATTGCATATTTCTTCATGTGACCAAAATATTTCAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGAATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATAAGAGAGATGAAGAGCAGCATCTTGAATCTCATACAGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGAACTTCTCCAGTGGCTTCTTCATTTCAGGGTA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_20	13	32906946	32907116	ACACTGACGACATGGTTCTACAATTCTTTGCCACGTATTTCTAGCC	TACGGTAGCAGAGACTTGGTCTTACCCTGAAATGAAGAAGCCACT	171	40	TTCTTGCAGTAAAGCAGGCAATATCTGGAACTTCTCCAGTGGCTTCTTCATTTTCAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAGAGACTTTCAATGCAAGTTTTTCAGGTCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_21	13	32907057	32907233	ACACTGACGACATGGTTCTACATTCTTGCAGTAAAGCAGGCAATA	TACGGTAGCAGAGACTTGGTCTGTCCACTTTCAGAGGCTTCAGTT	177	37	TCCAGTGGCTTCTTCATTTCAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAGAGACTTTCAATGCAAGTTTTTCAGGTCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACAGAAGGAGGACTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_22	13	32907091	32907270	ACACTGACGACATGGTTCTACATCCAGTGGCTTCTTCATTTCAGG	TACGGTAGCAGAGACTTGGTCTGAGTCCTCCTTCTGTGAGCAAAC	180	37	TGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_23	13	32907186	32907361	ACACTGACGACATGGTTCTACATGACTGATCCAAACTTTAAAAAGAAACT	TACGGTAGCAGAGACTTGGTCTAGTGGATATTAAACCTGCATTCTTCA	176	40	GAAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_24	13	32907264	32907455	ACACTGACGACATGGTTCTACAAGGACTCCTTATGTCCAAATTTAATTGAT	TACGGTAGCAGAGACTTGGTCTTTAGTTCTGATTTTTGGTCTTTCGG	192	32	AGGACTCCTTATGTCCAAATTTAATTGATAATGGAAGCTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTTAATATCCACTTTGAAAAAGAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAAAATAAAGGAAAAAAATACCGAAAGACCAAAAATCAGAACTAATTAACTGTTCAGCCCAGTTTGAAGCAAATGCTTTTGAAGCACCACTTACATTTGCAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_25	13	32907328	32907512	ACACTGACGACATGGTTCTACATGTAGCTTTGAAGAATGCAGGTTT	TACGGTAGCAGAGACTTGGTCTTTGCAAATGTAAGTGGTGCTTCA	185	30		

BRCA2	BRCA2_26	13	32907463	32907643	ACACTGACGACATGGTTCTACATTCAGCCCAGTTTGAAGCA	TACGGTAGCAGAGACTTGGTCTGATGATGCCTAAGATTAAATATAAGATATGAAGA	181	31	TTCAGCCCAGTTTGAAGCAAATGCTTTTGAAGCACCACTTACATTTGCAAATGCTGATTCAGGTACCTCTGTCTTTTTTTTTTTGTAAATAGTACATATAGTTTTATAGATGACGATTCCTTCTGTGTTTTTTTCTGCTTTTTAAAATCTTCATATCTTATATTTAATCTTAGGCATCATC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_27	13	32910305	32910494	ACACTGACGACATGGTTCTACAactgtgcccAAACACTACCTT	TACGGTAGCAGAGACTTGGTCTTCAGAATTGTCCCAAAAGAGCTA	190	33	actgtgcccAAACACTACCTTTTTAACTTAGTGAAAAATATTTAGTGAATGTGATTGATGGTACTTTAATTTTGTCACTTTGTGTTTTTATGTTTAGGTTTATTGCATTCTTCTGTGAAAAGAAGCTGTTCACAGAATGATTCTGAAGAACCAACTTTGTCCTTAACTAGCTCTTTTGGGACAATTCTGA	One primer sits in the repeat region
BRCA2	BRCA2_28	13	32910395	32910590	ACACTGACGACATGGTTCTACATGTTTAGGTTTATTGCATTCTTCTGTGA	TACGGTAGCAGAGACTTGGTCTACTGTAGTTTTTCCTTATTACATTTTGCT	196	32	TGTTTAGGTTTATTGCATTCTTCTGTGAAAAGAAGCTGTTCACAGAATGATTCTGAAGAACCAACTTTGTCCTTAACTAGCTCTTTTGGGACAATTCTGAGGAAATGTTCTAGAAATGAAACATGTTCTAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAATAAGGAAAAACTACAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_29	13	32910464	32910654	ACACTGACGACATGGTTCTACATCCTTAACTAGCTCTTTTGGGACA	TACGGTAGCAGAGACTTGGTCTGGATCATTTTCACACTGTCCTTCC	191	35	TCCTTAACTAGCTCTTTTGGGACAATTCTGAGGAAATGTTCTAGAAATGAAACATGTTCTAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAATAAGGAAAAACTACAGTTATTTATTACCCCAGAAGCTGATTCTCTGTCATGCCTGCAGGAAGGACAGTGTGAAAATGATCC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_30	13	32910603	32910766	ACACTGACGACATGGTTCTACACAGAAGCTGATTCTCTGTCATGC	TACGGTAGCAGAGACTTGGTCTACTTTTCTGGGATTGAAAGTCAGTAT	164	40	CAGAAGCTGATTCTCTGTCATGCCTGCAGGAAGGACAGTGTGAAAATGATCCAAAAAGCAAAAAAGTTTCAGATATAAAAGAAGAGGTCTTGGCTGCAGCATGTCACCCAGTACAACAATCCCAGAAAAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_31	13	32910671	32910842	ACACTGACGACATGGTTCTACATCAGATATAAAAGAAGAGGTCTTGGC	TACGGTAGCAGAGACTTGGTCTTGACTAGGTTTGACAGAACATCC	172	38	TCAGATATAAAAGAAGAGGTCTTGGCTGCAGCATGTCACCCAGTACAACATTCAAAAGTGGAATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAATGCCAGCACTCTTATTTTAACTCCTACTTCCAAGGATGTTCTGTCAAACC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_32	13	32910787	32910961	ACACTGACGACATGGTTCTACATGCCAGCACTCTTATTTTAACTCCT	TACGGTAGCAGAGACTTGGTCTAGCACATACATCTTGATTCTTTTCCA	175	35	TAGTCATGATTTCTAGAGGCAAAGAATCATACAAAATGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAATATTCCCATGGAAAAGAATCAAGATGTATGTGCT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_33	13	32910870	32911041	ACACTGACGACATGGTTCTACAAAATGTCAGACAAGCTCAAAGGT	TACGGTAGCAGAGACTTGGTCTTGTACCTTTCTTGAAGGTGATGCT	172	33	AAATGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAATATTCCCATGGAAAAGAATCAAGATGTATGTGCTTTAAATGAAAATTATAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATGAGAGTAGCATCACCTTCAAGAATGGTACAATTCAACCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_34	13	32910936	32911134	ACACTGACGACATGGTTCTACATGGAAAAGAATCAAGATGTATGTGCT	TACGGTAGCAGAGACTTGGTCTTCTTCAGAGTCTGGATTGACAGTTAT	199	32	TGGAAAAGAATCAAGATGTATGTGCTTTAAATGAAAATTATAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATGAGAGTAGCATCACCTTCAAGAAAGGTACAATTCAACCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGACAATGAGAATAATTTTG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_35	13	32911048	32911246	ACACTGACGACATGGTTCTACACCAAAACACAAATCTAAGAGTAATCCA	TACGGTAGCAGAGACTTGGTCTGTTTACACAAGTCAAGTCTGTTTCA	199	31	CCAAAACACAAATCTAAGAGTAATCCAAAAAAATCAAGAAGAAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAACTTTTCTCAGACAATGAGAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGCTTTAGGAAATACTAAGGAACTTCATGAAACAGACTTGACTTGTGTAAACGAACCCATTTTCAAGAACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAAGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_36	13	32911114	32911305	ACACTGACGACATGGTTCTACATGTCAATCCAGACTCTGAAGAACT	TACGGTAGCAGAGACTTGGTCTGCTTGTTTATCACCTGTGTCTCC	192	35	CAGACTTGACTTGTGTAAACGAACCCATTTTCAAGAACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAAGCAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAAATAGTGTAAAGCAGCATATAAAAATGATGTTCTTGCAGAGGAGAACAAAAATAGTGTAAAGCAGCATATAAAAATGACTCTAGGTCAAGATTTAAAATCGGACATCTCCTTGAATATAGATAAAATACCAGAAAAAAATAATGATTACATGAACAAATTCAAATCACAGTTTTGGAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_37	13	32911227	32911397	ACACTGACGACATGGTTCTACACAGACTTGACTTGTGTAAACGAACC	TACGGTAGCAGAGACTTGGTCTGACCTAGAGTCATTTTTATATGCTGCTTT	171	36	TTATATGGAGACACAGGTGATAAACAAGCAACCCAAGTGTCAATTAAAAAATATAAAAATGACTCTAGGTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_38	13	32911338	32911529	ACACTGACGACATGGTTCTACAATGTTCTTGCAGAGGAGAACAAA	TACGGTAGCAGAGACTTGGTCTAAGCTGTTCTGAAGCTACCTC	192	34	GAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAAGCAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_39	13	32911416	32911569	ACACTGACGACATGGTTCTACATCTCCTTGAATATAGATAAAATACCAGAAAAAA	TACGGTAGCAGAGACTTGGTCTTTCTTAATGTTATGTTCAGAGAGCTTG	154	33	TCTCCTTGAATATAGATAAAATACCAGAAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACAGTTTTGGAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAGAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_40	13	32911509	32911679	ACACTGACGACATGGTTCTACAGAGGTAGCTTCAGAACAGCTTCA	TACGGTAGCAGAGACTTGGTCTGAGGCTTGCTCAGTTTCTTTTGATT	171	34	GAGGTAGCTTCAGAACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAGCAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTCAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAGCAAAATGTTCTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_41	13	32911535	32911731	ACACTGACGACATGGTTCTACAAAGGAAATCAAGCTCTCTGAACA	TACGGTAGCAGAGACTTGGTCTTCAGAAACAACTACACTACTCTGTAAA	197	32	CAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATTGTAAATACCTTGGCATTAGATAATCAAAAGAAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGAGTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_42	13	32911651	32911821	ACACTGACGACATGGTTCTACAAGATAATCAAAAGAAACTGAGCAAGC	TACGGTAGCAGAGACTTGGTCTTCTGCCTTTTGGCTAGGTG	171	33	AGATAATCAAAAGAAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGAGTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_43	13	32911752	32911942	ACACTGACGACATGGTTCTACACCCCTCAGATGTTATTTTCCAAGC	TACGGTAGCAGAGACTTGGTCTAGTCATCTGGTTTTCAGGCACTT	191	35	CCCCTCAGATGTTATTTTCCAAGCAGGATTTTAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAATCAGGAAGTCAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAGTGCCTGAAAACCAGATGACT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_44	13	32911796	32911973	ACACTGACGACATGGTTCTACAAATTTAACACCTAGCCAAAAGGC	TACGGTAGCAGAGACTTGGTCTCTCTGCATTCCTCAGAAGTGGTC	178	35	AATTTAACACCTAGCCAAAAGGCAGAAATTACAGAACTTTCTACTATATTAGAAGAATCAGGAAGTCAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTA	Assays designed by relax mode and have no off-target hits

									CATATTGCAGAAGAGTACATTTGAAGTGCCTGAAAACCAGATGACTATCT TAAAGACCACTTCTGAGGAATGCAGAG	
BRCA2	BRCA2_45	13	32911913	32912084	ACACTGACGACATGGTTCTA CAACATTTGAAGTGCCTGAA AACCA	TACGGTAGCAGAGACTTGGTCTT TTTCAACAGGCCAGCAAACTTC	172	41	ACATTTGAAGTGCCTGAAAACCAGATGACTATCTTAAAGACCACTTCTGA GGAATGCAGAGATGCTGATCTTCATGTCATAATGAATGCCCCATCGATT GGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAAAC GGAAGTTTGCTGGCCTGTTGAAAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_46	13	32912025	32912218	ACACTGACGACATGGTTCTA CAGCAGCAAGCAATTTGAAG GTACA	TACGGTAGCAGAGACTTGGTCTA CTAAACAGTTTCACAGCTTTTTGC	194	38	GCAGCAAGCAATTTGAAGGTACAGTTGAAATTAAACGGAAGTTTGCTGG CCTGTTGAAAAATGACTGTAACAAAAGTGCTTCTGGTTATTTAACAGATG AAAATGAAGTGGGGTTTAGGGGCTTTTATTCTGCTCATGGCACAAAACT GAATGTTTCTACTGAAGCTCTGCAAAAAGCTGTGAAACTGTTTAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_47	13	32912129	32912305	ACACTGACGACATGGTTCTA CAGAAGTGGGGTTTAGGGG CTTTTA	TACGGTAGCAGAGACTTGGTCTT GAAACAACAGAATCATGACATTTA CTT	177	37	GAAGTGGGGTTTAGGGGCTTTTATTCTGCTCATGGCACAAAACTGAATG TTTCTACTGAAGCTCTGCAAAAAGCTGTGAAACTGTTTAGTGATATTGAG AATATTAGTGAGGAAACTTCTGCAGAGGTACATCCAATAAGTTTATCTTC AAGTAAATGTCATGATTCTGTTGTTTCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_48	13	32912216	32912409	ACACTGACGACATGGTTCTA CAAGTGATATTGAGAATATTA GTGAGGAAACT	TACGGTAGCAGAGACTTGGTCTA CAAAAGTGCCAGTAGTCATTTCA	194	27	AGTGATATTGAGAATATTAGTGAGGAAACTTCTGCAGAGGTACATCCAAT AAGTTTATCTTCAAGTAAATGTCATGATTCTGTTGTTTCAATGTTTAAGAT AGAAAATCATAATGATAAAACTGTAAGTGAAAAAAATAATAAATGCCAACT GATATTACAAAATAATATTGAAATGACTACTGGCACTTTTGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_49	13	32912285	32912479	ACACTGACGACATGGTTCTA CATGTCATGATTCTGTTGTTT CAATGT	TACGGTAGCAGAGACTTGGTCTT CTACTGGCAGCAGTATATTTGTT	195	26	TGTCATGATTCTGTTGTTTCAATGTTTAAGATAGAAAATCATAATGATAAA ACTGTAAGTGAAAAAAATAATAAATGCCAACTGATATTACAAAATAATATT GAAATGACTACTGGCACTTTTGTTGAAGAAATTACTGAAAATTACAAGAG AAATACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_50	13	32912391	32912574	ACACTGACGACATGGTTCTA CATGACTACTGGCACTTTTG TTGAAG	TACGGTAGCAGAGACTTGGTCTT GATCAGTAAATAGCAAGTCCGT	184	30	TGACTACTGGCACTTTTGTTGAAGAAATTACTGAAAATTACAAGAGAAAT ACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAATTCTCATAA CTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTCA TAAAGATGAAACGGACTTGCTATTTACTGATCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_51	13	32912431	32912629	ACACTGACGACATGGTTCTA CACAAGAGAAATACTGAAAA TGAAGATAACAAAT	TACGGTAGCAGAGACTTGGTCTC TGAGTGTTTCCCTCCTTCATAA	199	33	CAAGAGAAATACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGAA ATTCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTG TTTGTATTCATAAAGATGAAACGGACTTGCTATTTACTGATCAGCACAAC ATATGTCTTAAATTATCTGGCCAGTTTATGAAGGAGGGAAACACTCAG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_52	13	32912534	32912717	ACACTGACGACATGGTTCTA CATGTATTCATAAAGATGAAA CGGACTTG	TACGGTAGCAGAGACTTGGTCTA CTGTTCTTTATTTGAAGTATTACC ATGAC	184	34	TGTATTCATAAAGATGAAACGGACTTGCTATTTACTGATCAGCACAACAT ATGTCTTAAATTATCTGGCCAGTTTATGAAGGAGGGAAACACTCAGATTA AAGAAGATTTGTCAGATTTAACTTTTTTGGAAGTTGCGAAAGCTCAAGAA GCATGTCATGGTAATACTTCAAATAAAGAACAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_53	13	32912600	32912792	ACACTGACGACATGGTTCTA CAGGCCAGTTTATGAAGGAG GGAAA	TACGGTAGCAGAGACTTGGTCTT CCCACTTGCAGTCTGAAAAAATG	193	35	GGCCAGTTTATGAAGGAGGGAAACACTCAGATTAAAGAAGATTTGTCAG ATTTAACTTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCATGGTAAT ACTTCAAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAA AGATTTTGAGACTTCTGATACATTTTTTCAGACTGCAAGTGGGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_54	13	32912680	32912872	ACACTGACGACATGGTTCTA CAAGAAGCATGTCATGGTAA TACTTCAAA	TACGGTAGCAGAGACTTGGTCTA AAGTTATGCAATTCTTCTGGTTTC T	193	30	AGAAGCATGTCATGGTAATACTTCAAATAAAGAACAGTTAACTGCTACTA AAACGGAGCAAAATATAAAAGATTTTGAGACTTCTGATACATTTTTTCAGA CTGCAAGTGGGAAAAATATTAGTGTCGCCAAAGAGTCATTTAATAAAATT GTAAATTTCTTTGATCAGAAACCAGAAGAATTGCATAACTTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_55	13	32912788	32912986	ACACTGACGACATGGTTCTA CATGGGAAAAATATTAGTGT CGCCAAAG	TACGGTAGCAGAGACTTGGTCTA CCAACTGGGACACTTTCTTTCA	199	30	TGGGAAAAATATTAGTGTCGCCAAAGAGTCATTTAATAAAATTGTAAATTT CTTTGATCAGAAACCAGAAGAATTGCATAACTTTTCCTTAAATTCTGAATT ACATTCTGACATAAGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAA CAGACATAGTTAAACACAAAATACTGAAAGAAAGTGTCCCAGTTGGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_56	13	32912851	32913037	ACACTGACGACATGGTTCTA CAACCAGAAGAATTGCATAA CTTTTCCT	TACGGTAGCAGAGACTTGGTCTC TTTTCATCACGTTCGGGTTGTC	187	36	ACCAGAAGAATTGCATAACTTTTCCTTAAATTCTGAATTACATTCTGACAT AAGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTA AACACAAAATACTGAAAGAAAGTGTCCCAGTTGGTACTGGAAATCAACTA GTGACCTTCCAGGGACAACCCGAACGTGATGAAAAG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_57	13	32912966	32913164	ACACTGACGACATGGTTCTA CAAAAGAAAGTGTCCCAGTT GGT	TACGGTAGCAGAGACTTGGTCTT GGTGATTTCACTAGTACCTTGC	199	39	AAAGAAAGTGTCCCAGTTGGTACTGGAAATCAACTAGTGACCTTCCAGG GACAACCCGAACGTGATGAAAAGATCAAAGAACCTACTCTATTGGGTTTT CATACAGCTAGCGGGAAAAAAGTTAAAATTGCAAAGGAATCTTTGGACAA AGTGAAAAACCTTTTTGATGAAAAAGAGCAAGGTACTAGTGAAATCACCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_58	13	32913064	32913248	ACACTGACGACATGGTTCTA CATCATACAGCTAGCGGGAA AAAAGT	TACGGTAGCAGAGACTTGGTCTT GATCTCAATGGTCTCACATGCT	185	38	TCATACAGCTAGCGGGAAAAAAGTTAAAATTGCAAAGGAATCTTTGGACA AAGTGAAAAACCTTTTTGATGAAAAAGAGCAAGGTACTAGTGAAATCACC AGTTTTAGCCATCAATGGGCAAAGACCCTAAAGTACAGAGAGGCCTGTA AAGACCTTGAATTAGCATGTGAGACCATTGAGATCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_59	13	32913185	32913382	ACACTGACGACATGGTTCTA CAAAGACCCTAAAGTACAGA GAGGC	TACGGTAGCAGAGACTTGGTCTT GATGTTTTGAGATTTTCAGTTTGT CT	198	37	AAGACCCTAAAGTACAGAGAGGCCTGTAAAGACCTTGAATTAGCATGTG AGACCATTGAGATCACAGCTGCCCCAAAGTGTAAAGAAATGCAGAATTC TCTCAATAATGATAAAAACCTTGTTTCTATTGAGACTGTGGTGCCACCTA AGCTCTTAAGTGATAATTTATGTAGACAAACTGAAAATCTCAAAACATCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_60	13	32913301	32913486	ACACTGACGACATGGTTCTA CACCTTGTTTCTATTGAGACT GTGGTG	TACGGTAGCAGAGACTTGGTCTT CAATGACTGAATAAGGGGACTG	186	33	CCTTGTTTCTATTGAGACTGTGGTGCCACCTAAGCTCTTAAGTGATAATT TATGTAGACAAACTGAAAATCTCAAAACATCAAAAAGTATCTTTTTGAAAG TTAAAGTACATGAAAATGTAGAAAAAGAAACAGCAAAAAGTCCTGCAACT TGTTACACAAATCAGTCCCCTTATTCAGTCATTGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_61	13	32913356	32913547	ACACTGACGACATGGTTCTA CAAGACAAACTGAAAATCTC AAAACATCAAA	TACGGTAGCAGAGACTTGGTCTT GAAGTCTGACTCACAGAAGTTTT TC	192	32	AGACAAACTGAAAATCTCAAAACATCAAAAAGTATCTTTTTGAAAGTTAAA GTACATGAAAATGTAGAAAAAGAAACAGCAAAAAGTCCTGCAACTTGTTA CACAAATCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTA CACAAGTTGTAGTAGAAAAACTTCTGTGAGTCAGACTTCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_62	13	32913476	32913669	ACACTGACGACATGGTTCTA CATCAGTCATTGAAAATTCA GCCTTAGC	TACGGTAGCAGAGACTTGGTCTT CAGCTATAGTACTGTTTGAATTAT TTTCAT	194	31	TCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAA ACTTCTGTGAGTCAGACTTCATTACTTGAAGCAAAAAAATGGCTTAGAGA AGGAATATTTGATGGTCAACCAGAAAGAATAAATACTGCAGATTATGTAG GAAATTATTTGTATGAAAATAATTCAAACAGTACTATAGCTGA	Assays designed by relax mode and have no off-target hits

BRCA2	BRCA2_63	13	32913566	32913759	ACACTGACGACATGGTTCTACATGGCTTAGAGAAGGAATATTTGATGGT	TACGGTAGCAGAGACTTGGTCTACCTCATCAGAATGGTAGGAATAGC	194	31	TGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAAGAATAAATACTGCAGATTATGTAGGAAATTATTTGTATGAAAATAATTCAAACAGTACTATAGCTGAAAATGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCCTACCATTCTGATGAGGTTTCAAACAGTACTATAGCTGAAAATGACAAAAATCATCTCTCCGAAAAAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_64	13	32913649	32913831	ACACTGACGACATGGTTCTACATTCAAACAGTACTATAGCTGAAAATGAC	TACGGTAGCAGAGACTTGGTCTTCAACATTCTTCAATACTGGCTCAA	183	32	AAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCCTACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGCCAGTATTGAAGAATGTTGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_65	13	32913735	32913933	ACACTGACGACATGGTTCTACAGCTATTCCTACCATTCTGATGAGGT	TACGGTAGCAGAGACTTGGTCTACAAGTTCCTCAACGCAAATATC	199	32	GCTATTCCTACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAATAAACTTGATTCTGGTATTGAGCCAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAAAGATGCAAATGCATACCCACAAACTGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_66	13	32913854	32914036	ACACTGACGACATGGTTCTACATCCAAAGTAATATCCAATGTAAAAGATGC	TACGGTAGCAGAGACTTGGTCTACTGGCTATCCTAAATGCAGGTG	183	36	TCCAAAGTAATATCCAATGTAAAAGATGCAAATGCATACCCACAAACTGTAAATGAAGATATTTGCGTTGAGGAACTTGTAAAATAAAAATGCAGCCATTAAATTGTCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCATTTAGGATAGCCAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_67	13	32913964	32914149	ACACTGACGACATGGTTCTACATGCAGCCATTAAATTGTCCATATCT	TACGGTAGCAGAGACTTGGTCTTGGCAAATTTTTGATTTATTCTCGTTGTTT	186	32	TGCAGCCATTAAATTGTCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCATTTAGGATAGCCAGTGGTAAAATCGTTTGTGTTTCACATGAAACAATTAAAAAAGTGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGAAAACAACGAGAATAAATCAAAACAGACAGTTTCAGTAAAGTAATTAAGGAAAACAACGAGAATAAATCAAAAATTTGCCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_68	13	32914091	32914275	ACACTGACGACATGGTTCTACAACAGACAGTTTCAGTAAAGTAATTAAGGA	TACGGTAGCAGAGACTTGGTCTTCTTCACTCTGAATGTCAGCAAA	185	35	AATTTGCCAAACGAAAATTATGGCAGGTTGTTACGAGGCATTGGATGATTCAGAGGATATTCTTCATAACTCTCTAGATAATGATGAATGTAGCACGCATTCACATAAGGTTTTTGCTGACATTCAGAGTGAAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_69	13	32914156	32914353	ACACTGACGACATGGTTCTACAAATTATGGCAGGTTGTTACGAGG	TACGGTAGCAGAGACTTGGTCTGTTTCCAAACTAACATCACAAGGT	198	34	AATTATGGCAGGTTGTTACGAGGCATTGGATGATTCAGAGGATATTCTTCATAACTCTCTAGATAATGATGAATGTAGCACGCATTCACATAAGGTTTTTGCTGACATTCAGAGTGAAGAAATTTTACAACATAACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCACCTTGTGATGTTAGTTTGGAAAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_70	13	32914255	32914448	ACACTGACGACATGGTTCTACATGCTGACATTCAGAGTGAAGAAA	TACGGTAGCAGAGACTTGGTCTCAGATTTTCCACTTGCTGTGCTAA	194	34	TGCTGACATTCAGAGTGAAGAAATTTTACAACATAACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCACCTTGTGATGTTAGTTTGGAAACTTCAGATATATGTAAATGTAGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGGAAAATC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_71	13	32914397	32914568	ACACTGACGACATGGTTCTACAGTCTCATCTGCAAATACTTGTGGG	TACGGTAGCAGAGACTTGGTCTTGAGCTGGTCTGAATGTTCGTTA	172	37	GTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGGAAAATCTGTCCAGGTATCAGATGCTTCATTACAAAACGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCACGAACATTCAGACCAGCTCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_72	13	32914478	32914674	ACACTGACGACATGGTTCTACAGCAAGACAAGTGTTTTCTGAAATAGAAG	TACGGTAGCAGAGACTTGGTCTGCTGTACTAAATCCAGAGAAAGCAGA	197	35	GCAAGACAAGTGTTTTCTGAAATAGAAGATAGTACCAAGCAAGTCTTTTCCAAAGTATTGTTTAAAAGTAAAATACTGCTATACGTACTCCAGAACATTTAATATCCCAAAAAGGCTTTTCATATAATGTGGTAAATTCATCTGCTTTCTCTGGATTTAGTACAGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_73	13	32914546	32914737	ACACTGACGACATGGTTCTACATAACGAACATTCAGACCAGCTCA	TACGGTAGCAGAGACTTGGTCTTCCTCTAACACTCCCTTAACTTTGTG	192	36	TAACGAACATTCAGACCAGCTCACAAGAGAAGAAAATACTGCTATACGTACTCCAGAACATTTAATATCCCAAAAAGGCTTTTCATATAATGTGGTAAATTCATCTGCTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTTCCATTTTAGAAAGTTCCTTACACAAAGTTAAGGGAGTGTTAGAGGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_74	13	32914658	32914834	ACACTGACGACATGGTTCTACATCTGGATTTAGTACAGCAAGTGGA	TACGGTAGCAGAGACTTGGTCTTGGGTTTCTCTTATCAACACGAGG	177	36	TCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTTCCATTTTAGAAAGTTCCTTACACAAAGTTAAGGGAGTGTTAGAGGAAGTTTAATTATCAAATAACTTAGCATAGTCTTCACTATTCACCTACGTCTAGACAAAATGTATCAAAAATACTTCCTCGTGTTGATAAGAGAAACCCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_75	13	32914749	32914934	ACACTGACGACATGGTTCTACATCAGAACTGAGCATAGTCTTCACT	TACGGTAGCAGAGACTTGGTCTAGTGATTATTTTCTGAAGAACCACCTT	186	33	TCAGAACTGAGCATAGTCTTCACTATTCACCTACGTCTAGACAAAATGTATCAAAAATACTTCCTCGTGTTGATAAGAGAAACCCAGAGCACTGTGTAAACTCAGAAATGGAAAAAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_76	13	32914851	32915046	ACACTGACGACATGGTTCTACACAGAAATGGAAAAAACCTGCAGTA	TACGGTAGCAGAGACTTGGTCTGCCTGTTCTTTTCCCAAAACATGAA	196	32	CAGAAATGGAAAAAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACTCTATTAAAGTTTCTCCATATCTCTCAATTTCAACAAGACAAACAACAGTTGGTATTAGGAACCAAAGTGTCGTGTCACTTGTTGAGAACATTCATGTTTTGGGAAAAGAACAGGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_77	13	32914958	32915151	ACACTGACGACATGGTTCTACATCTCAATTTCAACAAGACAAACAACA	TACGGTAGCAGAGACTTGGTCTTCTGAATCTTTGGAGTAAGTAGAACA	194	33	TCTCAATTTCAACAAGACAAACAACAGTTGGTATTAGGAACCAAAGTGTCACTTGTTGAGAACATTCATGTTTTGGGAAAAGAACAGGCTTCACCTAAAAACGTAAAAATGGAAATTGGTAAAACTGAAACTTTTTCTGATGTTCCTGTGAAAAACAAATATAGAAGTTTGTTCTACTTACTCCAAAGATTCAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_78	13	32915045	32915243	ACACTGACGACATGGTTCTACAGCTTCACCTAAAAACGTAAAAATGGAA	TACGGTAGCAGAGACTTGGTCTGTGTGGCATGACTTGGCAGTTTA	199	34	GCTTCACCTAAAAACGTAAAAATGGAAATTGGTAAAACTGAAACTTTTTCTGATGTTCCTGTGAAAACAAATATAGAAGTTTGTTCTACTTACTCCAAAGATTCAGAAAACTACTTTGAAACAGAAGCAGTAGAAATTGCTAAAGCTTTTATGGAAGATGATGAACTGACAGATTCTAAACTGCCAAGTCATGCCACACAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_79	13	32915188	32915372	ACACTGACGACATGGTTCTACAAGCTTTTATGGAAGATGATGAACTGA	TACGGTAGCAGAGACTTGGTCTTAGTGATTGGCAACACGAAAGGT	185	38	AGCTTTTATGGAAGATGATGAACTGACAGATTCTAAACTGCCAAGTCATGCCACACATTCTCTTTTTACATGTCCCGAAAATGAGGAAATGGTTTTGTCAAATTCAAGAATTGGAAAAAGAAGAGGAGAGCCCCTTATCTTAGTGGGTAAGTGTTCATTTTTACCTTTCGTGTTGCCAATCACTA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_80	13	32918559	32918755	ACACTGACGACATGGTTCTACACACTATTTGTTGTAAGTATTTTTGTTTAACATTT	TACGGTAGCAGAGACTTGGTCTGCTTGATTTTCTATTATCCTGTCAAATTCAT	197	23	CACTATTTGTTGTAAGTATTTTTGTTTAACATTTAAAGAGTCAATACTTTAGCTTTAAAAAAATGGTCTATAGACTTTTGAGAAATAAAACTGATATTATTTGCCTTAAAAACATATATGAAATATTTCTTTTTAGGAGAACCCTCAATCAAAAGAAACTTATTAAATGAATTTGACAGGATAATAGAAAATCAAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_81	13	32918683	32918853	ACACTGACGACATGGTTCTACAATTTCTTTTTAGGAGAACCCTCAATCAA	TACGGTAGCAGAGACTTGGTCTGTCAGAATATTATATACCATACCTATAGAGGGAGA	171	29	ATTTCTTTTTAGGAGAACCCTCAATCAAAAGAAACTTATTAAATGAATTTGACAGGATAATAGAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT	Assays designed by relax mode and have no off-target hits

									CCAGATGGTAAAATTAGCTTTTTATTTATATCTGTTCTCCCTCTATAGGTA TGGTATATAATAttctgac	
BRCA2	BRCA2_83	13	32920895	32921044	ACACTGACGACATGGTTCTA CAGTATTTACAGTAACATGG ATATTCTCTTAGATTT	TACGGTAGCAGAGACTTGGTCTA CATGTCTTACCGAAAGGGTACA	150	31	GTATTTACAGTAACATGGATATTCTCTTAGATTTTAACTAATATGTAATATA AAATAATTGTTTCCTAGGCACAATAAAAGATCGAAGATTGTTTATGCATCA TGTTTCTTTAGAGCCGATTACCTGTGTACCCTTTCGGTAAGACATGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_127	13	32920953	32921102	ACACTGACGACATGGTTCTA CATTGTTTCCTAGGCACAAT AAAAGA	TACGGTAGCAGAGACTTGGTCTT GTTCATTTATAAAAACGAGACTTT TC	150	31	TTGTTTCCTAGGCACAATAAAAGATCGAAGATTGTTTATGCATCATGTTTC TTTAGAGCCGATTACCTGTGTACCCTTTCGGTAAGACATGTTTAAATTTTT CTAAATTCTAATACAGTATGAGAAAAGTCTCGTTTTTATAAATGAACA	
BRCA2	BRCA2_85	13	32928912	32929110	ACACTGACGACATGGTTCTA CACAAATGAGGGTCTGCAAC AAAGG	TACGGTAGCAGAGACTTGGTCTT GCTTGAAGATTTTTCCAAAGTCA G	199	35	CAAATGAGGGTCTGCAACAAAGGCATATTCCTAAATATTTATATGTGTAC TAGTCAATAAACTTATATATTTTCTCCCCATTGCAGCACAACTAAGGAAC GTCAAGAGATACAGAATCCAAATTTTACCGCACCTGGTCAAGAATTTCTG TCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_86	13	32928997	32929195	ACACTGACGACATGGTTCTA CAGCACAACTAAGGAACGTC AAGAG	TACGGTAGCAGAGACTTGGTCTG GTCTGCCTGTAGTAATCAAGTG	199	36	GCACAACTAAGGAACGTCAAGAGATACAGAATCCAAATTTTACCGCACC TGGTCAAGAATTTCTGTCTAAATCTCATTTGTATGAACATCTGACTTTGGA AAAATCTTCAAGCAATTTAGCAGTTTCAGGACATCCATTTTATCAAGTTTC TGCTACAAGAAATGAAAAAATGAGACACTTGATTACTACAGGCAGACC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_87	13	32929113	32929288	ACACTGACGACATGGTTCTA CATTAGCAGTTTCAGGACAT CCATT	TACGGTAGCAGAGACTTGGTCTT GTCTGTTTTCCTCCAAGTTAATAT TCC	176	35	TTAGCAGTTTCAGGACATCCATTTTATCAAGTTTCTGCTACAAGAAATGA AAAAATGAGACACTTGATTACTACAGGCAGACCAACCAAAGTCTTTGTTC CACCTTTTAAAACTAAATCACATTTTCACAGAGTTGAACAGTGTGTTAGG AATATTAACTTGGAGGAAAACAGACA	
BRCA2	BRCA2_88	13	32929181	32929377	ACACTGACGACATGGTTCTA CATACTACAGGCAGACCAAC CAAAG	TACGGTAGCAGAGACTTGGTCTT GGAGTTGTTTTTGTTAAACTGATG A	197	34	TACTACAGGCAGACCAACCAAAGTCTTTGTTCCACCTTTTAAAACTAAAT CACATTTTCACAGAGTTGAACAGTGTGTTAGGAATATTAACTTGGAGGAA AACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAA TAAGATTAATGACAATGAGATTCATCAGTTTAACAAAAACAACTCCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_89	13	32929315	32929467	ACACTGACGACATGGTTCTA CACTGATGATAGTAAAAATAA GATTAATGACAATGAG	TACGGTAGCAGAGACTTGGTCTA CTGAAAGGCAAAAATTCATCACA CA	153	31	CTGATGATAGTAAAAATAAGATTAATGACAATGAGATTCATCAGTTTAACA AAAACAACTCCAATCAAGCAGTAGCTGTAACTTTCACAAAGTGTGAAGAA GAACCTTTAGGTATTGTATGACAATTTGTGTGATGAATTTTTGCCTTTCAG T	
BRCA2	BRCA2_90	13	32930503	32930690	ACACTGACGACATGGTTCTA CAGGCCAGGGGTTGTGCTTT TTA	TACGGTAGCAGAGACTTGGTCTT TCGAGGCAGAGTGGATGTTTTT	188	37	ggccAGGGGTTGTGCTTTTTAAATTTCAATTTTATTTTTGCTAAGTATTTATT CTTTGATAGATTTAATTACAAGTCTTCAGAATGCCAGAGATATACAGGAT ATGCGAATTAAGAAGAAACAAAGGCAACGCGTCTTTCCACAGCCAGGCA GTCTGTATCTTGCAAAAACATCCACTCTGCCTCGAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_91	13	32930607	32930790	ACACTGACGACATGGTTCTA CATGCGAATTAAGAAGAAAC AAAGGC	TACGGTAGCAGAGACTTGGTCTA CACTCTGTCATAAAAGCCATCAG T	184	45	TGCGAATTAAGAAGAAACAAAGGCAACGCGTCTTTCCACAGCCAGGCAG TCTGTATCTTGCAAAAACATCCACTCTGCCTCGAATCTCTCTGAAAGCAG CAGTAGGAGGCCAAGTTCCCTCTGCGTGTTCTCATAAACAGGTATGTGT TTGTCTACAATACTGATGGCTTTTATGACAGAGTGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_92	13	32931809	32932007	ACACTGACGACATGGTTCTA CATTGTTTTTATTGTGTGATA CATGTTTACTTT	TACGGTAGCAGAGACTTGGTCTA GCCAACTGTATTCCTTTTCCAGT	199	30	TTGTTTTTATTGTGTGATACATGTTTACTTTAAATTGTTTTTCTTTTTTGTG TGTGTTTATTTTGTGTAGCTGTATACGTATGGCGTTTCTAAACATTGCATA AAAATTAACAGCAAAAATGCAGAGTCTTTTCAGTTTCACACTGAAGATTAT TTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGCT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_93	13	32931907	32932099	ACACTGACGACATGGTTCTA CAGCATAAAAATTAACAGCA AAAATGCAG	TACGGTAGCAGAGACTTGGTCTA AAGTTAACACACAATCTTTTTGCA TAG	193	36	GCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTCAGTTTCACACTGAA GATTATTTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGC TGATGGTGGATGGCTCATACCCTCCAATGATGGAAAGGCTGGAAAAGAA GAATTTTATAGGTACTCTATGCAAAAAGATTGTGTGTTAACTTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_94	13	32936578	32936771	ACACTGACGACATGGTTCTA CATGTACAGAGAATAGTTGT AGTTGTTGA	TACGGTAGCAGAGACTTGGTCTA GGAAAGGCACATTCCATAGCTG	194	36	TGTACAGAGAATAGTTGTAGTTGTTGAATTCAGTATCATCCTATGTGGTT TTTATGATAATATTCTACTTTTATTTGTTCAGGGCTCTGTGTGACACTCCA GGTGTGGATCCAAAGCTTATTTCTAGAATTTGGGTTTATAATCACTATAG ATGGATCATATGGAAACTGGCAGCTATGGAATGTGCCTTTCCT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_95	13	32936661	32936831	ACACTGACGACATGGTTCTA CAGCTCTGTGTGACACTCCA GGT	TACGGTAGCAGAGACTTGGTCTC CTGTATTTTAGTTGAAGAAGCAC CC	171	41	GCTCTGTGTGACACTCCAGGTGTGGATCCAAAGCTTATTTCTAGAATTTG GGTTTATAATCACTATAGATGGATCATATGGAAACTGGCAGCTATGGAAT GTGCCTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCCAGAAAGGGT GCTTCTTCAACTAAAATACAGG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_96	13	32936738	32936933	ACACTGACGACATGGTTCTA CAATGGAAACTGGCAGCTAT GGAAT	TACGGTAGCAGAGACTTGGTCTG ACAACTGGCTTGTGCAACATTT	196	40	ATGGAAACTGGCAGCTATGGAATGTGCCTTTCCTAAGGAATTTGCTAATA GATGCCTAAGCCCAGAAAGGGTGCTTCTTCAACTAAAATACAGGCAAGT TTAAAGCATTACATTACGTAATCATATACGGCAGTATGGTTAAGGTTTCT GTGTAGTCTGTGACTTCCATGTCAAAATGTTGCACAAGCCAGTTGTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_97	13	32937263	32937433	ACACTGACGACATGGTTCTA CATGGAATTCTAGAGTCACA CTTCCTAA	TACGGTAGCAGAGACTTGGTCTT GCGCTCAATGAAATTATGTCAGA AAC	171	35	TGGAAATTCTAGAGTCACACTTCCTAAAATATGCATTTTTGTTTTCACTTTT AGATATGATACGGAAATTGATAGAAGCAGAAGATCGGCTATAAAAAAGAT AATGGAAAGGGATGACACAGCTGCAAAAACACTTGTTCTCTGTGTTTCTG ACATAATTTCATTGAGCGCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_98	13	32937366	32937563	ACACTGACGACATGGTTCTA CATGGAAAGGGATGACACAG C	TACGGTAGCAGAGACTTGGTCTT CTTTAAGACAGCTAAGAGGGGAG	198	40	TGGAAAGGGATGACACAGCTGCAAAAACACTTGTTCTCTGTGTTTCTGA CATAATTTCATTGAGCGCAAATATATCTGAAACTTCTAGCAATAAAACTAG TAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGG TATGCTGTTAAGGCCCAGTTAGATCCTCCCCTCTTAGCTGTCTTAAAGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_99	13	32937465	32937648	ACACTGACGACATGGTTCTA CAGTAGTGCAGATACCCAAA AAGTGG	TACGGTAGCAGAGACTTGGTCTG CTTCAAGAGGTGTACAGGCATC	184	47	GTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTG GTATGCTGTTAAGGCCCAGTTAGATCCTCCCCTCTTAGCTGTCTTAAAGA ATGGCAGACTGACAGTTGGTCAGAAGATTATTCTTCATGGAGCAGAACT GGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_100	13	32937594	32937785	ACACTGACGACATGGTTCTA CATTCTTCATGGAGCAGAAC TGGTG	TACGGTAGCAGAGACTTGGTCTT CAGTACATCTAAGAAATTGAGCA TCC	192	35	TTCTTCATGGAGCAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCT TGAAGCCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTTGG TAAAAATCAGTCATTGATTCAGTTAAATTCTAGAAGTTTTACATTTAAATTT TAAATGCTTACTAAGGATGCTCAATTTCTTAGATGTACTGA	
BRCA2	BRCA2_101	13	32944423	32944616	ACACTGACGACATGGTTCTA CATTTTTAAAGTGAATATTTT TAAGGCAGTTCT	TACGGTAGCAGAGACTTGGTCTC AGAGGAAAAGGTCTAGGGTCAG	194	32	TTTTTAAAGTGAATATTTTTAAGGCAGTTCTAGAAGAATGAAAACTCTTAT GATATCTGTAATAGAATTGAATACATATTTAACTACTAAATCAATATATTTA	Assays designed by relax mode and have no off-target hits

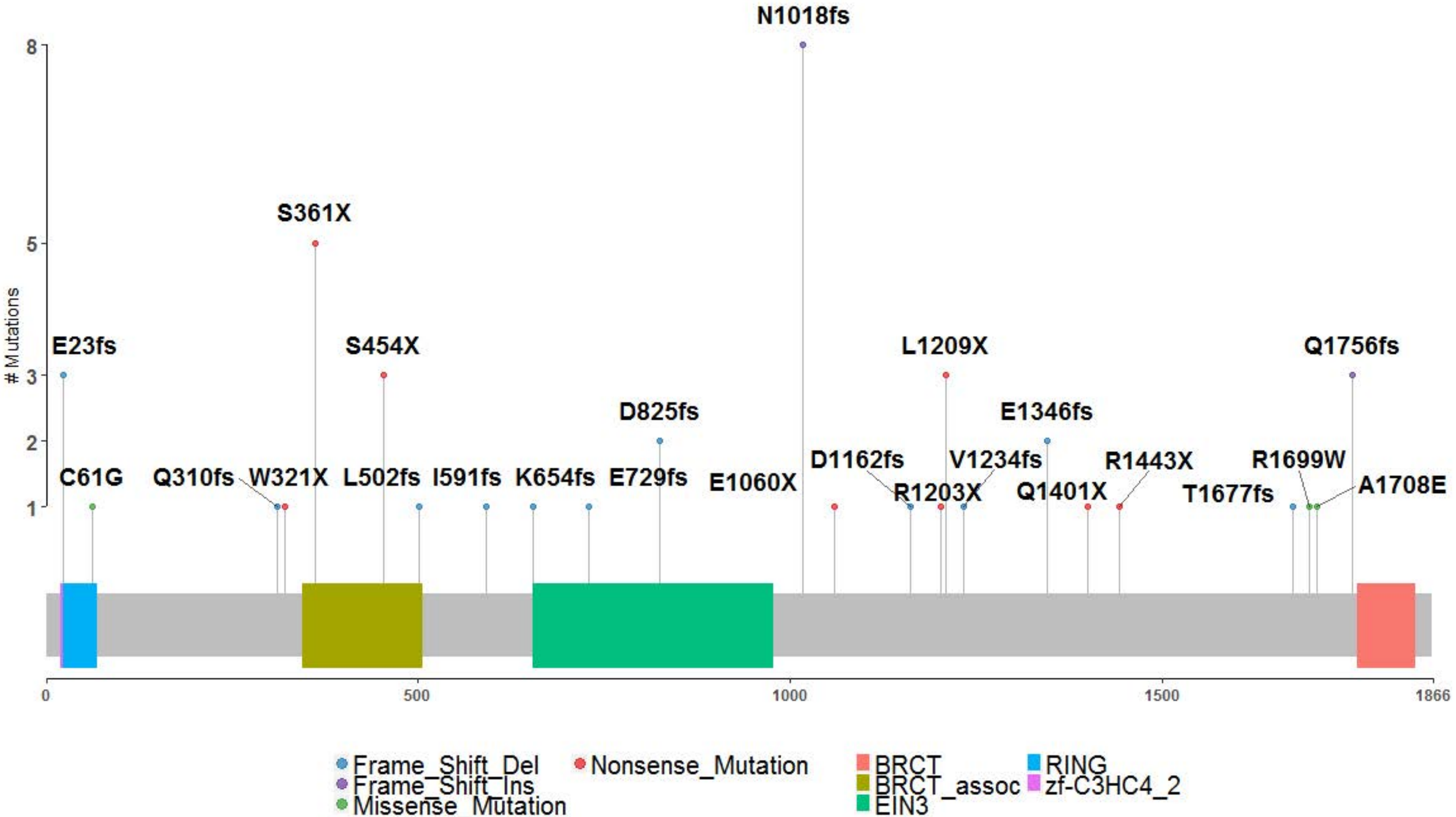
									TTAATTTGTCCAGATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAACTTGGATTCTTTCCTGACCCTAGACCTTTTCCTCTG	
BRCA2	BRCA2_102	13	32944558	32944739	ACACTGACGACATGGTTCTACAGGCCTGCTCGCTGGTAT	TACGGTAGCAGAGACTTGGTCTATCAAAAGAAAGAAATATATGGTAAGTTTCAAG	182	39	GGCCTGCTCGCTGGTATACCAAACTTGGATTCTTTCCTGACCCTAGACCTTTTCCTCTGCCCTTATCATCGCTTTTCAGTGATGGAGGAAATGTTGGTTGTGTTGATGTAATTATTCAAAGAGCATACCCTATACAGGTATGATGTATTCTTGAAACTTACCATATATTTCTTTCTTTTGAT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_103	13	32945018	32945192	ACACTGACGACATGGTTCTACACTGTGCCTGGCCTGATACAATTA	TACGGTAGCAGAGACTTGGTCTCTAGTCTCTTTTGTTGGGCCTCC	175	38	ctgtgcctggccTGATACAATTAACTTGAATGTTATATATGTGACTTTTTTGGTGTGTGTAACACATTATTACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTCGCAATGAAAGAGAGGAAGAAAAGGAAGCAGCAAAATATGTGGAGGCCCAACAAAAGAGACTAG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_104	13	32945088	32945279	ACACTGACGACATGGTTCTACATACAGTGGATGGAGAAGACATCA	TACGGTAGCAGAGACTTGGTCTTCATATTAGAAATAACAATGTGTACCATATAACT	192	34	TACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTCGCAATGAAAGAGAGGAAGAAAAGGAAGCAGCAAAATATGTGGAGGCCCAACAAAAGAGACTAGAAGCCTTATTCACTAAAATTCAGGAGGAATTTGAAGAACATGAAGGTAAAATTAGTTATATGGTACACATTGTTATTTCTAATATGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_105	13	32950735	32950927	ACACTGACGACATGGTTCTACATGCTTGGTTCTTTAGTTTTAGTTGCT	TACGGTAGCAGAGACTTGGTCTTCAAGGTAAGCTGGGTCTGC	193	37	TGCTTGGTTCTTTAGTTTTAGTTGCTTTTGAATTTACAGTTTAGTGAATTAATAATCCTTTTGTTTTCTTAGAAAACACAACAAAACCATATTTACCATCACGTGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCCAGCTTACCTTGA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_106	13	32950838	32951010	ACACTGACGACATGGTTCTACATGCACTAACAAGACAGCAAGTTC	TACGGTAGCAGAGACTTGGTCTCCTGTGATGGCCAGAGAGTCTAA	173	45	TGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCCAGCTTACCTTGAAGTAAGAGGACATATAATGAGGCTTGATGATTATTCAAGGTGAGAAGCTGTTTTAGACTCTCTGGCCATCACAGG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_107	13	32953398	32953576	ACACTGACGACATGGTTCTACAAGATGGAACTTTTTTGTTCTGATTGC	TACGGTAGCAGAGACTTGGTCTTTCCTTTTGTTCAGCAGATTCCA	179	36	AGATGGAACTTTTTTGTTCTGATTGCTTTTTATTCCAATATCTTAAATGGTCACAGGGTTATTTCAGTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAACAAGCTCAGATCCAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAGGAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_108	13	32953496	32953694	ACACTGACGACATGGTTCTACAAGGCAAATGTTGAATGATAAGAAACA	TACGGTAGCAGAGACTTGGTCTAAGTTAATAAAACTGATAAAAACAAAGCATTTAC	199	35	AGGCAAATGTTGAATGATAAGAAACAAGCTCAGATCCAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAAGAAAAAGATTCAGGTAAGTATGTAAATGCTTTGTTTTTATCAGTTTTATTAACTT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_109	13	32953847	32954025	ACACTGACGACATGGTTCTACACACTTCTTCCATTGCATCTTTCTCA	TACGGTAGCAGAGACTTGGTCTTTTGTCGCTGCTAACTGTATGTT	179	34	CACTTCTTCCATTGCATCTTTCTCATCTTTCTCCAAACAGTTATACTGAGTATTTGGCGTCCATCATCAGATTTATATTCTCTGTTAACAGAAGGAAAGAGATACAGAATTTATCATCTTGCAACTTCAAAATCTAAAAGTAAATCTGAAAGAGCAGCTAACATACAGTTAGCAGCGACAAA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_110	13	32953901	32954099	ACACTGACGACATGGTTCTACATGGCGTCCATCATCAGATTTATATTC	TACGGTAGCAGAGACTTGGTCTACTAACAAGCACTTATCAAAACTGAAA	199	33	TGGCGTCCATCATCAGATTTATATTCTCTGTTAACAGAAGGAAAGAGATACAGAATTTATCATCTTGCAACTTCAAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAAAAACTCAGTATCAACAACTACCGGTACAAACCTTTCATTGTAATTTTTCAGTTTTGATAAGTGCTTGTTA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_111	13	32954047	32954235	ACACTGACGACATGGTTCTACAACCGGTACAAACCTTTCATTGT	TACGGTAGCAGAGACTTGGTCTGAACAAGATGGCTGAAAGTCTGG	189	35	ACCGGTACAAACCTTTCATTGTAATTTTTCAGTTTTGATAAGTGCTTGTTAGTTTATGGAATCTCCATATGTTGAATTTTTGTTTTGTTTTCTGTAGGTTTCAGATGAAATTTTATTTCAGATTTACCAGCCACGGGAGCCCCTTCACTTCAGCAAATTTTTAGATCCAGACTTTCAGCCATCTTGTTC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_112	13	32954171	32954369	ACACTGACGACATGGTTCTACATACCAGCCACGGGAGCC	TACGGTAGCAGAGACTTGGTCTTGGTAGCTCCAACTAATCATAAGAGA	199	35	TACCAGCCACGGGAGCCCCTTCACTTCAGCAAATTTTTAGATCCAGACTTTCAGCCATCTTGTTCTGAGGTGGACCTAATAGGATTTGTCGTTTCTGTTGTGAAAAAAACAGGTAATGCACAATATAGTTAATTTTTTTTATTGATTCTTTTAAAAAACATTGTCTTTTAAAATCTCTTATGATTAGTTGGAGCTACCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_Intron_24__region_1__1	13	32955429	32955627	ACACTGACGACATGGTTCTACAGGGGAGGGAGATTACAAACAAAG	TACGGTAGCAGAGACTTGGTCTACCTCACTCCCTCAATTCCTTCA	199	40	ggggagggagattacaaacaaagaaataagtaatatacatgtgtatagttttttagtgctcagaaaaaaaattaagtgggtaaggggggtaatgtcagagaagagagagggatgtaatttagattgagaggtgaggagagagacctccctggaaagctgacatttgagtgaagcttgaaggaattgagggagtgaggt	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__2	13	32955521	32955716	ACACTGACGACATGGTTCTACATGTCAGAGAAGAGAGAGGGATGT	TACGGTAGCAGAGACTTGGTCTCAATGCTTCACGGCACACTAGG	196	49	tgtcagagaagagagagggatgtaattttagattgagaggtgaggagagagacctccctggaaagctgacatttgagtgaagcttgaaggaattgagggagtgaggtgaggcatgtggccatctggggaaagctttccaggcaattacaaaggccgcagtacagcaggatcatgcctagtgtgccgtgaagcattg	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__3	13	32955600	32955779	ACACTGACGACATGGTTCTACAAAGCTTGAAGGAATTGAGGGAGT	TACGGTAGCAGAGACTTGGTCTCACACGACCTGGCTCTTCAC	180	53	aagcttgaaggaattgagggagtgaggtgaggcatgtggccatctggggaaagctttccaggcaattacaaaggccgcagtacagcaggatcatgcctagtgtgccgtgaagcattggcagagaccagagagtgagaagtaacatccagggacagaggcagtgaagagccaggtcgtgtg	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__4	13	32955731	32955909	ACACTGACGACATGGTTCTACAGTGAGAAGTAACATCCAGGGACA	TACGGTAGCAGAGACTTGGTCTCCCCTACAGCCTATTCTCAACAC	179	51	gtgagaagtaacatccagggacagaggcagtgaagagccaggtcgtgtgggggtccttgtgtggactgtaacttcctgtgatgacaggaagtcacaggaaaattccaggtagagggacactgtctgacaggttttcacagaatcattcaggccactgtgttgagacaggaaaattccaggtagagggacactgtctgacaggttttcacagaatcattcaggccactgtgttgagaatggcttgaggggcacaagagtacaaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaaaataggaattgccacttagaaggaaagactgcaagaaaagca	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__5	13	32955824	32956006	ACACTGACGACATGGTTCTACAACAGGAAAATTCCAGGTAGAGGG	TACGGTAGCAGAGACTTGGTCTGACTGCTTCTCACCACTTCCATT	183	45	aataggctgtaggggggcacaagagtacaaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaaaataggaattgccacttagaaggaaagactgcaagaaaagcagtggtgagaagcagtcagattcttgttgtattttgaaggtaggggggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaaggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaaagcaagtatgtggggaagttcaggagctcagttttagacagttaagttttagatgcttattaggcatctaagtagaaatgtctacttgatggttacataggaatctgttcagaggaatggctgg	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__6	13	32955922	32956107	ACACTGACGACATGGTTCTACAAAACAAGCCATTTGGAGGCTCTT	TACGGTAGCAGAGACTTGGTCTTGCTTTTCTTGCAGTCTTTCCTT	186	42	aaacaagccatttggaggctctttcaagcacttaggcaaaagatgatgaaccaaacaaaagcaatggaagtggtgagaagcagtcagattcttgttgtattttgaaggtaggggggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagca	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_1__7	13	32956034	32956227	ACACTGACGACATGGTTCTACAGGGACGGTGCAGGATGG	TACGGTAGCAGAGACTTGGTCTCCAGCCATTCCTCTGAACAGATT	194	42	gggacggtgcaggatggtctgaacattgggaaaaatggaattgccacttagaaggaaagactgcaagaaaagcaaagcaagtatgtggggaagttcaggagctcagttttagacagttaagttttagatgcttattaggcatctaagtagaaatgtctacttgatggttacataggaatctgttcagaggaatggctgg	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_2__1	13	32958725	32958923	ACACTGACGACATGGTTCTACAAAGTGAGGAGGCCTAGATGTCAG	TACGGTAGCAGAGACTTGGTCTTCTGGTCCAAGACTCTGTTTTCC	199	43	AAGTGAGGAGGCCTAGATGTCAGAGGAGTCCGGCTAAACCACTGCAGAACTGCTGCCTAATTCACAGCAACCATGAGTAAAAATGCTGATGATCATCAGGGTCAAGGATAGTCTGGAGCAGTTAAGATGTTACTTTACATGGGAGGTATCAATTAAAGATGATGAAATGCCTGATTTGGAAAACAGAGTCTTGGACCAGA	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_2__2	13	32958830	32959024	ACACTGACGACATGGTTCTACAGATAGTCTGGAGCAGTTAAGATGT	TACGGTAGCAGAGACTTGGTCTAGTTCTCCAGCACTTCCTCATTC	195	41	GATAGTCTGGAGCAGTTAAGATGTTACTTTACATGGGAGGTATCAATTAAAGATGATGAAATGCCTGATTTGGAAAACAGAGTCTTGGACCAGATTGGG	Two primers sits in the repeat region

									TTTCTAGACTAAATACAGTGTGGGAATACACAATACACAACCTACTAGCC TATGTGAAACACCCGAAAGGCCAGAATGAGGAAGTGCTGGAGAACT	
BRCA2	BRCA2_Intron_24__region_2__3	13	32958974	32959172	ACACTGACGACATGGTTCTACATAGCCTATGTGAAACACCCGAAA	TACGGTAGCAGAGACTTGGTCTGCAAATGTTCTCTACCTTGTCCA	199	47	TAGCCTATGTGAAACACCCGAAAGGCCAGAATGAGGAAGTGCTGGAGA ACTTGAAAGAAGCTGAAGACTTAATCCAGAAAGAAGATGCCAATCAGATT TGAGAAGCCTGGTAACCTGGGGCAACTTTGCCTGGGTGTATTACCACAT GGGCAGACTGGCAGAAACCCAGACTTACCTGGACAAGGTAGAGAACAT TTGC	
BRCA2	BRCA2_Intron_24__region_2__4	13	32959058	32959234	ACACTGACGACATGGTTCTACAATGCCAATCAGATTTGAGAAGCC	TACGGTAGCAGAGACTTGGTCTTCTTCCTCACAGTCCATCTCTGG	177	47	ATGCCAATCAGATTTGAGAAGCCTGGTAACCTGGGGCAACTTTGCCTGG GTGTATTACCACATGGGCAGACTGGCAGAAACCCAGACTTACCTGGACA AGGTAGAGAACATTTGCAAGAAGTTTTCAAGTCCTTTCTGTCACAGAATG GAATGTCCAGAGATGGACTGTGAGGAAGA	
BRCA2	BRCA2_Intron_24__region_2__5	13	32959147	32959333	ACACTGACGACATGGTTCTACAACCTGGACAAGGTAGAGAACATT	TACGGTAGCAGAGACTTGGTCTGTGTTGAGTTCAGGGTTTTCAGC	187	48	ACCTGGACAAGGTAGAGAACATTTGCAAGAAGTTTTCAAGTCCTTTCTGT CACAGAATGGAATGTCCAGAGATGGACTGTGAGGAAGAACGGGCCTTG CTGGAATGTGGAGGGAAGAATTATGAACAGGCCAAGGCCTGCTTTGAAA AGGATCTGGCAGTGGCTGCTGAAAACCCTGAACTCAACAC	
BRCA2	BRCA2_Intron_24__region_2__6	13	32959205	32959401	ACACTGACGACATGGTTCTACAGGAATGTCCAGAGATGGACTGTG	TACGGTAGCAGAGACTTGGTCTAAAATGACTTGTGATCCCCCGTT	197	50	GGAATGTCCAGAGATGGACTGTGAGGAAGAACGGGCCTTGCTGGAATG TGGAGGGAAGAATTATGAACAGGCCAAGGCCTGCTTTGAAAAGGATCTG GCAGTGGCTGCTGAAAACCCTGAACTCAACACTGGGTATGAAATCACCG CCTGTCGCCTGGATGGCTTTAAATTAGCAACGGGGGATCACAAGTCATT TT	
BRCA2	BRCA2_Intron_24__region_2__7	13	32959311	32959504	ACACTGACGACATGGTTCTACAGCTGAAAACCCTGAACTCAACAC	TACGGTAGCAGAGACTTGGTCTCCTTCAGCTTCCTGTCCTTCATC	194	47	GCTGAAAACCCTGAACTCAACACTGGGTATGAAATCACCGCCTGTCGCC TGGATGGCTTTAAATTAGCAACGGGGGATCACAAGTCATTTTCTTTGCCT ACCCTAAGGCAGGCTGTCAGGCTAAATGTAGATGATAGATATAGTAAGG TTCTTCTTGCCCTGAAGCTTTGGGATGAAGGACAGGAAGCTGAAGG	
BRCA2	BRCA2_Intron_24__region_3__1	13	32964498	32964682	ACACTGACGACATGGTTCTACAGCGGCTCGCAAGGCTA	TACGGTAGCAGAGACTTGGTCTACAAAGAAGATTTTTAAAGGTAGGAAGCA	185	32	gcggctcgcaaggctaggagtttgggacaagtctgggcaacagtgagattctgtctctataaacataaaaaCTAAATTTAAAAAAAAAACTACTTTAAAACATAATAATAAAACAAACTGTACAAGTTCATATTCCTGATGCATGATAACATTTAATgcttcctacctttaaaaatcttctttgt	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_Intron_24__region_3__2	13	32964614	32964772	ACACTGACGACATGGTTCTACAACTGTACAAGTTCATATTCCTGATGC	TACGGTAGCAGAGACTTGGTCTAAGCATCTGACTAGGGAGGTAAT	159	35	ACTGTACAAGTTCATATTCCTGATGCATGATAACATTTAATgcttcctaccttaaaaatcttctttgttttgcatagatgctcttttgttctccccctcttgatgaatttgtcctattcattattcagctcaagtattacctccctagtcagatgcttacagtctgggttcccctagtcagatgctt	One primer sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__3	13	32964707	32964900	ACACTGACGACATGGTTCTACACCCCCTCTTGATGAATTTGTCCT	TACGGTAGCAGAGACTTGGTCTACTGAGGCTAGTAGGTGGCTTAT	194	44	cccccttgatgaatttgtcctattcattattcagctcaagtattacctccctagtcagatgcttacagtctgggttagatcctcctcctccagcttttgaagcattttgttggtttggctgtttcagcacttgtcacatggtccatgatcctactctgtacacttctgaataagccacctactagcctcagt	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__4	13	32964809	32965000	ACACTGACGACATGGTTCTACAAAGCATTTTGTTGGTTTGGCTGT	TACGGTAGCAGAGACTTGGTCTCCTGGAGTTTTCAACAACTGACC	192	44	aagcattttgttggtttggctgtttcagcacttgtcacatggtccatgatcctacctgtacacttctgaataagccacctactagcctcagtaatacaatgatctcttcaaggacagggactctgtttGGATTTCTACTTCCACTTCTGACATAATGGGTTGAAGCAGGGGTCAGTTGTTGAAAACTCCAGG	One primer sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__5	13	32964908	32965094	ACACTGACGACATGGTTCTACATGATCTCTTCAAGGACAGGGACT	TACGGTAGCAGAGACTTGGTCTTAACCTCTCTGAGCTCCAGTTTC	187	44	tgatctcttcaaggacagggactctgtttGGATTTCTACTTCCACTTCTGACATAATGGGTTGAAGCAGGGGTCAGTTGTTGAAAACTCCAGGTatgcagcatctcatacggtcctcatagtcacactgttcatttgctattatcatcccactttacagatggggaaactggagctcagagaggtta	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__6	13	32965017	32965207	ACACTGACGACATGGTTCTACACGGTCCTCATAGTCACACTGTTC	TACGGTAGCAGAGACTTGGTCTTGAGTTTGCTTTTGTTTTGTCAGC	191	40	cggtcctcatagtcacactgttcatttgctattatcatcccactttacagatggggaaactggagctcagagaggttaagtagcctgctcagggtcacaatgctataaattgatttgaacttatactttcaggccctaaagctcttaggttctttcttatacttcatgctgACAAAACAAAAGCAAACTCA	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__7	13	32965060	32965244	ACACTGACGACATGGTTCTACATTTACAGATGGGGAAACTGGAGC	TACGGTAGCAGAGACTTGGTCTTACAGATGTCCCTGTTTTAAGCC	185	39	tttacagatggggaaactggagctcagagaggttaagtagcctgctcagggtcacaatgctataaattgattgaacttatactttcaggccctaaagctcttaggttctttcttatacttcatgctgACAAAACAAAAGCAAACTCAACATTTGAGAGTTGGGCTTAAAACAGGGACATCTGTAtgctgACAAAACAAAAGCAAACTCAACATTTGAGAGTTGGGCTTAAAACAG	One primer sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__8	13	32965183	32965359	ACACTGACGACATGGTTCTACAtgctgACAAAACAAAAGCAAACT	TACGGTAGCAGAGACTTGGTCTgaaACAGGCTTTCCCCAAAACAA	177	34	GGACATCTGTATTTTTAATCTAATGCTTTGTTACTGTATTACAGAAACACTGTGATATATAATGAGTTAATTAAACGAGAACCTTTCTTAGGTTGGGAAAGATTTGTTTTGGGGAAAGCCTGTttc	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__9	13	32965220	32965418	ACACTGACGACATGGTTCTACATGGGCTTAAAACAGGGACATCTG	TACGGTAGCAGAGACTTGGTCTGCTGTTCCTAAGGGCATTTTCTA	199	36	TGGGCTTAAAACAGGGACATCTGTATTTTTAATCTAATGCTTTGTTACTGTATTACAGAAACACTGTGATATATAATGAGTTAATTAAACGAGAACCTTTCTTAGGTTGGGAAAGATTTGTTTTGGGGAAAGCCTGTttccctgggaaacagacttacagatttcatgtaggagattagaaaatgcccttaggaacagc	One primer sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__10	13	32965331	32965527	ACACTGACGACATGGTTCTACAAAAGATTTGTTTTGGGGAAAGCC	TACGGTAGCAGAGACTTGGTCTCAGGCTAGCAAGACTCTGAAGG	197	47	AAAGATTTGTTTTGGGGAAAGCCTGTTtccctgggaaacagacttacagatttcatgtaggagattagaaaatgcccttaggaacagcacttgtgaggaagcaaatgcagcaggattgggcagaagaagaagaaaggttcagttagtcccacagggacttctggagctgggtggcccttcagagtcttgctagcctgcagcaggattgggcagaagaagaagaaaggttcagttagtcccacagggacttctggagctgggtggcccttcagagtcttgctagcctgaggcaagagccagtccttgcatactggctcctccagggaggggcatagccttaagcaagacaatgcctttcgacagagggcaagtccaggagggaactcagagcagagggcaagtccaggagggaactcagaggtgagttgtcaatagctagctctccccagaagctggagcatcacatgccttggtcctgaaggggatctgcacccgcaccatggcatccacTCCAGctggaggatcacatgccttggtcctgaaggggatctgcacccgcaccatggcatccacTCCAGGTG	Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__11	13	32965437	32965630	ACACTGACGACATGGTTCTACAGCAGCAGGATTGGGCAGAAG	TACGGTAGCAGAGACTTGGTCTCTCTGAGTTCCCTCCTGGACTTG	194	56		Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__12	13	32965531	32965725	ACACTGACGACATGGTTCTACACAAGAGCCAGTCCTTGCATACT	TACGGTAGCAGAGACTTGGTCTCTGGAGTGGATGCCATGGTG	195	56		Two primers sits in the repeat region
BRCA2	BRCA2_Intron_24__region_3__13	13	32965663	32965858	ACACTGACGACATGGTTCTACACTGGAGGATCACATGCCTTGG	TACGGTAGCAGAGACTTGGTCTTATTTTGCAGCTTTGTGGTCTGG	196	43	GAATCGGTGACAGTGGTTTTATAAATTGCTAAGTCCTTTATTGTTTCAGTGACATTTTCTAAAAGGAATTAAAAGCTTTGAAGAATTCTATGCAAGTTCAGAGTAGGCCAGACCACAAAGCTGCAAAATA	One primer sits in the repeat region
BRCA2	BRCA2_113	13	32968741	32968935	ACACTGACGACATGGTTCTACAAGGCATATTAGAGTTTCCTTTCTTGC	TACGGTAGCAGAGACTTGGTCTTGCAGCAATTAACATATGAGGCTT	195	32	AGGCATATTAGAGTTTCCTTTCTTGCATCTTAAAATTCATCTAACACATCTATAATAACATTCTTTTCTTTTTTTTCCATTCTAGGACTTGCCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_114	13	32968830	32969028	ACACTGACGACATGGTTCTACATGCCCCTTTCGTCTATTTGTCAG	TACGGTAGCAGAGACTTGGTCTGCCCTCTTTTGGACTAGCAGAA	199	40	TGCCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCACTGCAAGCAACCTCCAGTGGCGACCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTTCTGTGTTTTCTGCTAGTCCAAAAGAGGGC	Assays designed by relax mode and have no off-target hits

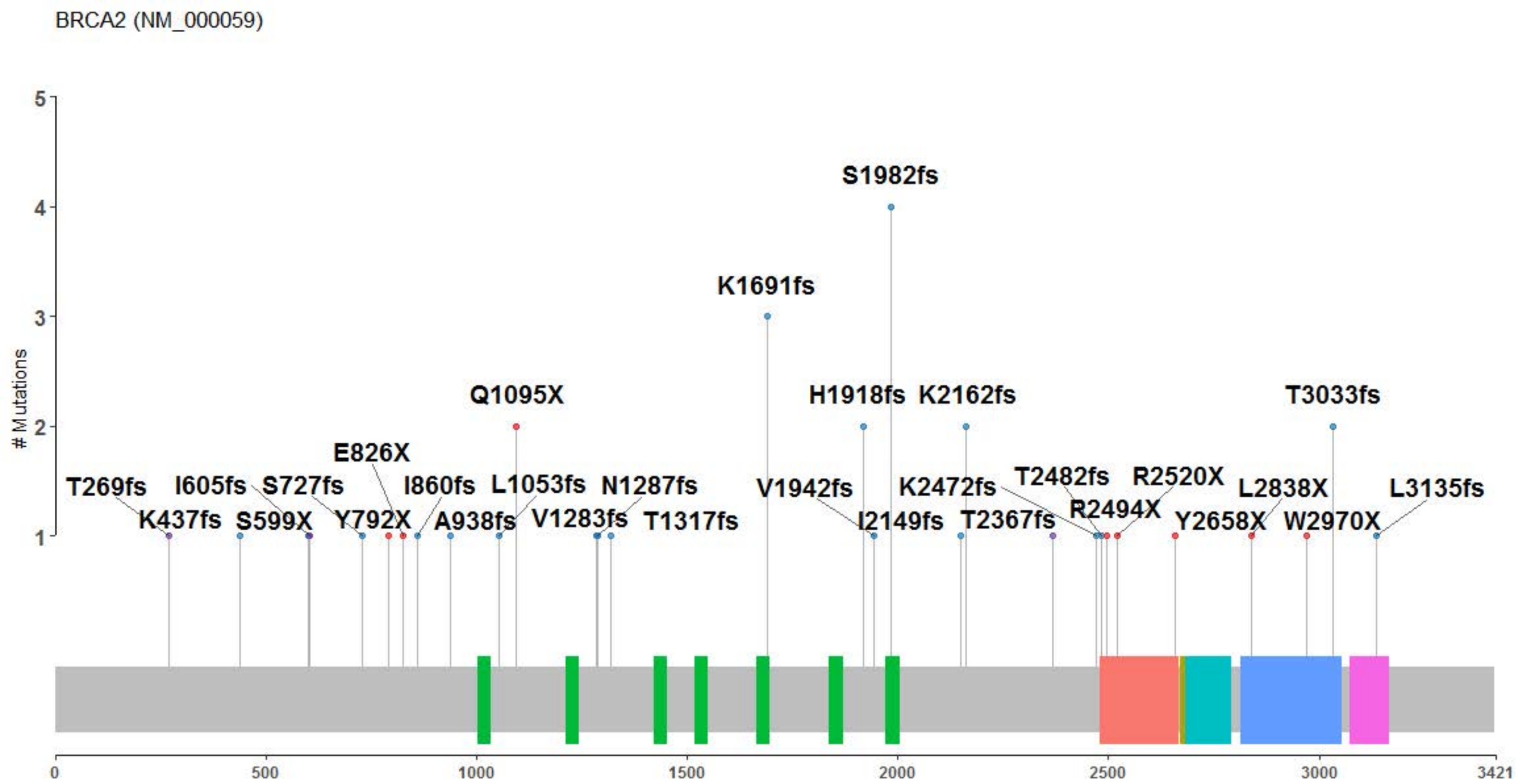
BRCA2	BRCA2_115	13	32968930	32969107	ACACTGACGACATGGTTCTACAGCTGCAAGCAACCTCCAGT	TACGGTAGCAGAGACTTGGTCTTACCAAAATGTGTGGTGATGCTG	178	41	GCTGCAAGCAACCTCCAGTGGCGACCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTTCTGTGTTTTCTGCTAGTCCAAAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAATACTGTTGAGGTAAGGTTACTTTTCAGCATCACCACACATTTTGGTA	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_116	13	32970934	32971113	ACACTGACGACATGGTTCTACATGGTCCAAACTTTTCATTTCTGCTTT	TACGGTAGCAGAGACTTGGTCTGGGTGGACCACTTGGGA	180	34	TGGTCCAAACTTTTCATTTCTGCTTTTAAAGGAAATACTTTTGGAAACATAAATATGTGGGTTTGCAATTTATAAAGCAGCTTTTCCACTTATTTTCTTAGAATATTGACATACTTTGCAATGAAGCAGAAAACAAGCTTATGCATATACTGCATGCAAATGATCCCAAGTGGTCCAC	
BRCA2	BRCA2_117	13	32971050	32971232	ACACTGACGACATGGTTCTACATGCAATGAAGCAGAAAACAAGC	TACGGTAGCAGAGACTTGGTCTTGGCCTCCATATATACTTCTTATAATATTCC	183	40	TGCAATGAAGCAGAAAACAAGCTTATGCATATACTGCATGCAAATGATCCCAAGTGGTCCACCCCAACTAAAGACTGTACTTCAGGGCCGTACACTGCTCAAATCATTCCTGGTACAGGAAACAAGCTTCTGGTAAGTTAATGTAAACTCAAGGAATATTATAAGAAGTATATATGGAGGCCA	
BRCA2	BRCA2_118	13	32972189	32972375	ACACTGACGACATGGTTCTACAACTGTGTGTAATATTTGCGTGCTT	TACGGTAGCAGAGACTTGGTCTGTGGAAACAGACTTCCTTTTGGC	187	29	ACTGTGTGTAATATTTGCGTGCTTAAATATTTTCAATGAAAAGTTACTTTGATTTAGTTTTTTATGTTACTACATAATTATGATAGGCTACGTTTTCATTTTTTTATCAGATGTCTTCTCCTAATTGTGAGATATATTATCAAAGTCCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_119	13	32972289	32972464	ACACTGACGACATGGTTCTACATTTTTATCAGATGTCTTCTCCTAATTGTG	TACGGTAGCAGAGACTTGGTCTCCAAGGCTCTTCTCTTTTTGCAG	176	39	TTTTTATCAGATGTCTTCTCCTAATTGTGAGATATATTATCAAAGTCCTTTATCATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTGTCTCAGCCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAGAACTGCAAAAAGAGAAGAGCCTTGG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_120	13	32972412	32972609	ACACTGACGACATGGTTCTACAAGGGGAGAAAGAGATTGATGACC	TACGGTAGCAGAGACTTGGTCTGGAGAATTCAGTTCTTTTTTCTTTATGGG	198	43	AGGGGAGAAAGAGATTGATGACCAAAAGAACTGCAAAAAGAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTTTCTCCGGCTGCACAGAAGGCATTTCAGCCACCAAGGAGTTGTGGCACCAAATACGAAACACCCATAAAGAAAAAAGAACTGAATTCTCCTACCTCCACCTGTTAGTCCCATTTGTACATTTGTTTCTCCGGCTGCACAG	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_121	13	32972486	32972684	ACACTGACGACATGGTTCTACATACCTCCACCTGTTAGTCCCATT	TACGGTAGCAGAGACTTGGTCTGCAAGTTCTTCGTCAGCTATTGA	199	39	AAGGCATTTCAGCCACCAAGGAGTTGTGGCACCAAATACGAAACACCCATAAAGAAAAAAGAACTGAATTCTCCTCAGATGACTCCATTTAAAAAATTCAATGAAATTTCTCTTTTGGAAAGTAATTCAATAGCTGACGAAGAACTTGC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_122	13	32972573	32972771	ACACTGACGACATGGTTCTACAACGAAACACCCATAAAGAAAAAGAACT	TACGGTAGCAGAGACTTGGTCTGTGGGAGCAGTCCTAGTGGAT	199	35	ACGAAACACCCATAAAGAAAAAGAACTGAATTCTCCTCAGATGACTCCATTTAAAAAATTCAATGAAATTTCTCTTTTGGAAAGTAATTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAAACAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCCAC	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_123	13	32972696	32972846	ACACTGACGACATGGTTCTACACCCAAGCTCTTTTGTCTGGTTC	TACGGTAGCAGAGACTTGGTCTGCCTGGGAACTCTCCTGTTCT	151	44	CCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAAACAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCCACCAGTTCAGAAGATTATCTCAGACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGC	
BRCA2	BRCA2_124	13	32972756	32972954	ACACTGACGACATGGTTCTACACTAGGACTGCTCCCACCA	TACGGTAGCAGAGACTTGGTCTACTGGAAAGGTTAAGCGTCAATA	199	40	CTAGGACTGCTCCCACCAGTTCAGAAGATTATCTCAGACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATTTGCAAAGGCGACAATAAATTATTGACGCTTAACCTTTCCAGT	Assays designed by relax mode and have no off-target hits
BRCA2	BRCA2_3_UTR_1	13	32972832	32972989	ACACTGACGACATGGTTCTACAGGAGAGTTCCCAGGCCAGTA	TACGGTAGCAGAGACTTGGTCTAATGTGTGGTTTGAAATTATATTCCAGT	158	35	GGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATTTGCAAAGGCGACAATAAATTATTGACGCTTAACCTTTCCAGTTTATAAGACTGGAATATAATTTCAAACCACCACACATT	
BRCA2	BRCA2_3_UTR_2	13	32972934	32973106	ACACTGACGACATGGTTCTACATTGACGCTTAACCTTTCCAGTTT	TACGGTAGCAGAGACTTGGTCTTGCAACTGAAGCAAAAGTATACCA	173	35	TTGACGCTTAACCTTTCCAGTTTATAAGACTGGAATATAATTTCAAACCACACATTAGTACTTATGTTGCACAATGAGAAAAGAAATTAGTTTCAAATTTACCTCAGCGTTTGTGTATCGGGCAAAAATCGTTTTGCCCGATTCCGTATTGGTATACTTTTGCTTCAGTTGCA	
BRCA2	BRCA2_3_UTR_3	13	32973032	32973229	ACACTGACGACATGGTTCTACATTACCTCAGCGTTTGTGTATCGG	TACGGTAGCAGAGACTTGGTCTCTGGCCTCAAGCACTCCTC	198	42	TTACCTCAGCGTTTGTGTATCGGGCAAAAATCGTTTTGCCCGATTCCGTATTGGTATACTTTTGCTTCAGTTGCATATCTTAAAACTAAATGTAATTTATTAACTAATCAAGAAAAACATCTTTggctgagctcggtggctcatgcctgtaatcccaacactttgagaagctgaggtgggaggagtgcttgaggccag	One primer sits in the repeat region
BRCA2	BRCA2_3_UTR_5	13	32973253	32973427	ACACTGACGACATGGTTCTACACATAGGGAGACCCCCATCTT	TACGGTAGCAGAGACTTGGTCTTCTGCATCAAAATAACTGTACTAAGAGA	175	30	cataggggagaccccatctttacaaagaaaaaaaaaaGGGGAAAAGAAAATCTTTTAAATCTTTGGATTTGATCACTACAAGTATTATTTTACAAGTGAAATAAACATACCATTTTCTTTTAGATTGTGTCATTAAATGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGA	One primer sits in the repeat region
BRCA2	BRCA2_3_UTR_6	13	32973316	32973499	ACACTGACGACATGGTTCTACATGGATTTGATCACTACAAGTATTATTTTACA	TACGGTAGCAGAGACTTGGTCTAGGAGAACTATTTCATAGTGAGTTACC	184	29	TGGATTTGATCACTACAAGTATTATTTTACAAGTGAAATAAACATACCATTTTCTTTTAGATTGTGTCATTAAATGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGATAATTCCTTTTAGTTTAGCTACTATTTTAGGGGATTTTTTTTTAGAGGTAACTCACTATGAAATAGTTCTCCT	
BRCA2	BRCA2_3_UTR_7	13	32973390	32973583	ACACTGACGACATGGTTCTACATGGAATGAGGTCTCTTAGTACAGTT	TACGGTAGCAGAGACTTGGTCTTGCTCAAAAGGAAACACCACTCT	194	34	TGGAATGAGGTCTCTTAGTACAGTTATTTTGATGCAGATAATTCCTTTTAGTTTAGCTACTATTTTAGGGGATTTTTTTTTAGAGGTAACTCACTATGAAATAGTTCTCCTTAATGCAAATATGTTGGTTCTGCTATAGTTCCATCCTGTTCAAAAGTCAGGATGAATATGAAGAGTGGTGTTTCCTTTTGAGCA	
BRCA2	BRCA2_3_UTR_8	13	32973511	32973681	ACACTGACGACATGGTTCTACATGTTGGTTCTGCTATAGTTCCATCC	TACGGTAGCAGAGACTTGGTCTTTTAATTTCAGAGATCACACTGGAATAGT	171	35	TGTTGGTTCTGCTATAGTTCCATCCTGTTCAAAAGTCAGGATGAATATGAAGAGTGGTGTTTCCTTTTGAGCAATTCTTCATCCTTAAGTCAGCATGATTATAAGAAAAATAGAACCCTCAGTGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAA	
BRCA2	BRCA2_3_UTR_9	13	32973572	32973770	ACACTGACGACATGGTTCTACATCCTTTTGAGCAATTCTTCATCCTT	TACGGTAGCAGAGACTTGGTCTTGAGTTTGGATGACCATTTTGTTG	199	27	TCCTTTTGAGCAATTCTTCATCCTTAAGTCAGCATGATTATAAGAAAAATAGAACCCTCAGTGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAATTACTTCAACTAAAAATTCAAATACTTTAAATCAGAAGATTTCAAGTTAATTTATTTTTTTTTTCAACAAAATGGTCATCCAAACTCA	

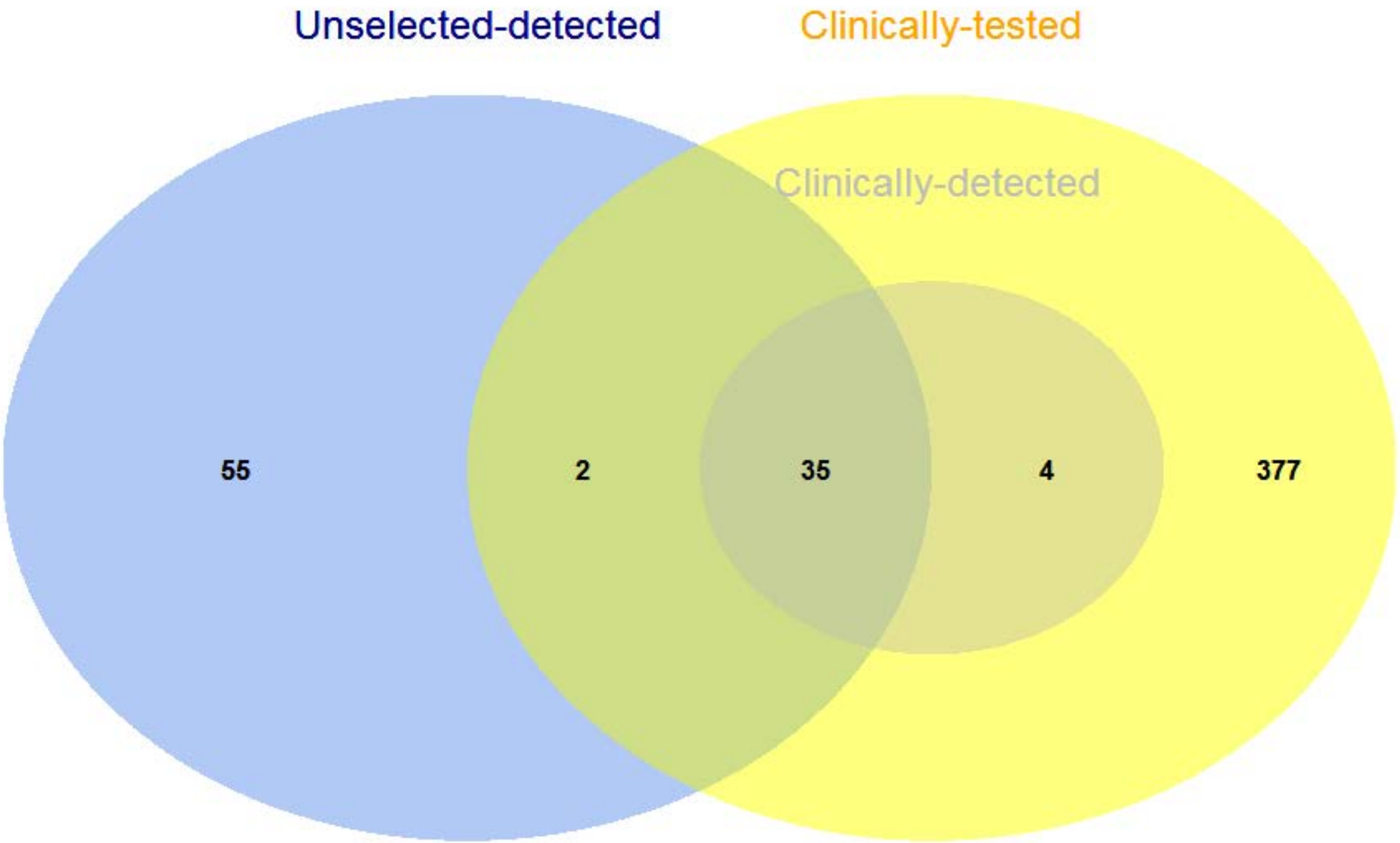
BRCA2	BRCA2_3_UTR_10	13	32973633	32973831	ACACTGACGACATGGTTCTACATGTAACTCTAATTCCTTTTTACTATTCCAGT	TACGGTAGCAGAGACTTGGTCTGCGCTAAAAATAAAGCAGGCAGA	199	28	TGTAACTCTAATTCCTTTTTACTATTCCAGTGTGATCTCTGAAATTAAATTACTTCAACTAAAAATTCAAATACTTTAAATCAGAAGATTTCATAGTTAATTTATTTTTTTTTTCAACAAAATGGTCATCCAAACTCAAACTTGAGAAAATATCTTGCTTTCAAATTGGCACTGATTCTGCCTGCTTTATTTTTAGCGC	
BRCA2	BRCA2_3_UTR_11	13	32973746	32973929	ACACTGACGACATGGTTCTACATCAACAAAATGGTCATCCAAACTCAA	TACGGTAGCAGAGACTTGGTCTaaaaaGGACGTAACAAATGAGAGTAT	184	35	TCAACAAAATGGTCATCCAAACTCAAACTTGAGAAAATATCTTGCTTTCAAATTGGCACTGATTCTGCCTGCTTTATTTTTAGCGCTATCACAGGACCCAGAGCCTATGCCCTTTTAAACTTACCACAAAAGCAGAAGATTAATTCAATTTAAGATGATACTCTCATTTGTTACGTCCttttt	One primer sits in the repeat region
BRCA2_3_UTR	BRCA2_3_UTR_12	13	32973158	32973307	ACACTGACGACATGGTTCTACACTGAGCTCGGTGGCTCAT	TACGGTAGCAGAGACTTGGTCTAAAGATTTTCTTTTCCCCTTTTT	150	49	CTGAGCTCGGTGGCTCATGCCTGTAATCCCAACACTTTGAGAAGCTGAGGTGGGAGGAGTGCTTGAGGCCAGGAGTTCAAGACCAGCCTGGGCAACATAGGGAGACCCCCATCTTTACAAAGAAAAAAAAAAGGGGAAAAGAAAATCTTT	
BRCA2_Promoter_Combined	BRCA2_Promoter_Combined_14	13	32888661	32888849	ACACTGACGACATGGTTCTACACTGCGAGGAAGACAGGTGAT	TACGGTAGCAGAGACTTGGTCTGCACGGCTAACTTTGCATTT	189	55	CTGCGAGGAAGACAGGTGATCCGAATCCTAAGAATGCAAAAGATGGGCCGGGTGTGGTGGCTCATGCCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCACCTGAGGTCGGGAGGTTGAGACCAGACTGACCAACAACGGAGAAACCCCGTCTCTACTTAAAAATGCAAAGTTAGCCGTGC	
BRCA2_Promoter_Combined	BRCA2_Promoter_Combined_15	13	32888792	32888990	ACACTGACGACATGGTTCTACAAGACTGACCAACAACGGAGAA	TACGGTAGCAGAGACTTGGTCTTGAGACGGAGTTTCGCTCTT	199	57	AGACTGACCAACAACGGAGAAACCCCGTCTCTACTTAAAAATGCAAAGTTAGCCGTGCGTGGTGGCCCATGCCTGTATTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAACCACTTGATCCCTGGAGGCGGAAGTTGCGGTGAGCGGAGATTGCGCCATTGCACACCAGCCCGGGCCACAAGAGCGAAACTCCGTCTCA	
BRCA2_Promoter_Combined	BRCA2_Promoter_Combined_16	13	32888925	32889092	ACACTGACGACATGGTTCTACAGTTGCGGTGAGCGGAGAT	TACGGTAGCAGAGACTTGGTCTCCGTTTCCTTGCTTGAAAAA	168	50	GTTGCGGTGAGCGGAGATTGCGCCATTGCACACCAGCCCGGGCCACAAGAGCGAAACTCCGTCTCAAAAAAAAAAAGCAAAAGATACTACCAAGCCCTGCGGAGCAAGGTACCTCACACTTCATGAGCGAGTTAAGATGGGTTTCACAATTTTTCAAGCAAGGAAACGG	

BRCA1 (NM_007294)



BRCA2 (NM_000059)




Unselected-detected
Clinically-tested
Clinically-detected
55
2
35
4
377